

FIGURE 1

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGAC
TGCAGACTAAACCAGTCATTACTGTTCAAGAGCGTTCTGCTAATCTACACTTTATTTTC
TGGATCACTGGCGTTATCCTTCTGCAGTTGGCATTGGGGCAAGGTGAGCCTGGAGAATT
CTTTCTCTTAAATGAGAAGGCCACCAATGTCCCCTCGTGCTCATTGCTACTGGTACCG
TCATTATTCTTTGGCACCTTGGTTGTTGCTACCTGCCGAGCTCTGCATGGATGCTA
AAACTGTATGCAATGTTCTGACTCTCGTTGGTGAACTGGTCGTGCCATCGTAGG
ATTGTTTCAGACATGAGATTAAGAACAGCTTAAGAATAATTATGAGAAGGCTTGAAGC
AGTATAACTCTACAGGAGATTATAGAACGCATGCAGTAGACAAGATCCAAATACGTTGCAT
TGTTGTGGTGTCAACGATTATAGAGATTGGACAGATACTAATTACTCAGAAAAAGGATT
TCCTAACAGAGTTGCTGTAAAACTTGAAAGATTGTACTCCACAGAGAGATGCAGACAAAGTAAACA
ATGAAGGTTGTTATAAAGGTGATGACCATTATAGAGTCAGAAATGGAGTCGTTGCAGGA
ATTTCCTTGGAGTTGCTTGCCTCCAACTGATTGGAATCTTCTCGCCTACTGCCWCTCTCG
TGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCCCTCT
CTACCTTAAGGACATTAGGGTCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTG
ACAACACTACTTACTGATAGACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTAT
GTAGACCTAAAACTACACCAATAGGCTGATTCAATCAAGATCCGTGCTCGCAGTGGCTGAT
TCAATCAAGATGTATGTTGCTATGTTCTAAGTCCACCTCTATCCCATTCAATGTTAGATCG
TTGAAACCTGTATCCCTGAAACACTGGAAGAGCTAGTAAATTGTAATGAAGT

FIGURE 2

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><MW: -1, pI: 8.36, NX(S/T): 1
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VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV
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Important features of the protein:

Signal peptide:

amino acids 1-42

Transmembrane domains:

amino acids 19-42, 61-83, 92-114, 209-230,

N-glycosylation site.

amino acids 134-138

Tyrosine kinase phosphorylation site.

amino acids 160-168, 160-169

N-myristoylation site.

amino acids 75-81, 78-84, 210-216, 214-220, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 69-80, 211-222

FIGURE 3

FIGURE 4

MIVFGWAVFLASRSLGQGLLTLEEHIAHFLGTGGAATTMGNSCICRDDSGTDDSVDTQQQQ
AENSAVPTADTRSQPRDPVRPPRRGRGPHEPRRKKQNVDGLVLDTLAVIRTLVDKO

Signal peptide:

amino acids 1-16

Casein kinase II phosphorylation site.

amino acids 22-26, 50-54, 113-117

N-myristoylation site.

amino acids 18-24, 32-38, 34-40, 35-41, 51-57

FIGURE 5

GGCAGGCGCTGTCCACCCGGGGCGTGGGAGTGAGGTACCAAGATTCAAGCCCATTGGCC
CCGACGCCTCTGTTCTCGGAATCCGGGTGCTGCGGATTGAGGTCCCGTTCTAACGGACTG
CAAG**ATG**GAGGAAGGCGGGAACCTAGGAGGCCTGATTAAGATGGTCATCTACTGGTCTTGT
CAGGTGCCTGGGCATGCAAATGTGGGTGACCTTCGTCTCAGGCTTCTGCTTTCCGAAGC
CTTCCCCGACATACCTTCGGACTAGTGCAGAGCAAACCTCTCCCCCTCTACTTCCACATCTC
CATGGGCTGTGCCTTCATCAACCTCTGCATCTGGCTTCACAGCATGCTTGGGCTCAGCTCA
CATTCTGGGAGGCCAGCCAGCTTACCTGCTGTTCCCTGAGCCTTACGCTGGCCACTGTCAAC
GCCCGCTGGCTGGAACCCCGCACACAGCTGCCATGTGGGCCCTGCAAACCGTGGAGAAGGA
GCGAGGCCTGGGTGGGGAGGTACCAGGCAGCCACCAGGGTCCCGATCCCTACCGCCAGCTGC
GAGAGAAGGACCCAAGTACAGTGCTCTCCGCCAGAATTCTCCGCTACCATGGGCTGTCC
TCTCTTGCAATCTGGCTGCGTCTGAGCAATGGGCTCTGTCTCGCTGGCCTGCCCTGGA
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AAAAAAAAAAAAA

FIGURE 6

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GLGGEVPGSHQGPDPYRQLREKDPKYSALRQNFFRYHGLSSLCNLGCVLSNGLCLAGLALEIRSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 86-103, 60-75

Casein kinase II phosphorylation site.

amino acids 82-86

Tyrosine kinase phosphorylation site.

amino acids 144-151

N-myristoylation site.

amino acids 4-10, 5-11, 47-53, 170-176, 176-182

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 54-65

G-protein coupled receptors proteins.

amino acids 44-85

FIGURE 7

AATTCA GATTTAAGCCCATTCTGCAGTGGAA T T CATGA ACTAGCAAGAGGGACACC AT CTT
 CTTGTATTATA CAAGAAAGGAGTGTA CCTATCACACACAGGGGGAAA **ATG** CTCTTTGGGT
 GCTAGGCCTCCTAATCCTCTGGTTCTGTGGACTCGTAAAGGAAA ACTAAAGATTGAAG
 ACATCACTGATAAGTACATTTTATCACTGGATGTGACTCGGGCTTGGAAACTTGGCAGCC
 AGAACCTTGATAAAAAGGGATTCATGTAATCGCTGCCTGTCTGACTGAATCAGGATCAAC
 AGCTTAAAGGCAGAACCTCAGAGAGACTTCGTACTGTGCTCTGGATGTGACCGACCCAG
 AGAATGTCAAGAGGACTGCCAGGGTGAAGAACCAAGTTGGGAGAAAGGTCTCTGGGT
 CTGATCAATAATGCTGGTGTCCCGCGTGTGGCTCCACTGACTGGCTGACACTAGAGGA
 CTACAGAGAACCTATTGAAGTGAACCTGTTGGACTCATCAGTGTGACACTAAATATGCTTC
 CTTGGTCAAGAAAGCTCAAGGGAGAGTTATTAATGTCTCCAGTGTGGAGGTGCCTTGCA
 ATCGTTGGAGGGGGCTATACTCCATCAAATATGCAGTGGAAAGGTTCAATGACAGCTTAAG
 ACGGGACATGAAAGCTTTGGTGTGCACGTCTCATGCATTGAACCAGGATTGTTCAAAACAA
 ACTTGGCAGATCCAGTAAAGGTAAATTGAAAAAAACTGCCATTGGAGCAGCTGTCTCCA
 GACATCAAACAACAATATGGAGAAGGTTACATTGAAAAAAAGTCTAGACAAACTGAAAGGCAA
 TAAATCCTATGTGAACATGGACCTCTCCGGTGGTAGAGTGCATGGACCACGCTCTAACAA
 GTCTCTCCCTAAGACTCATTATGCCGCTGGAAAAGATGCCAAATTTCTGGATACCTCTG
 TCTCACATGCCAGCAGCTTGCAAGACTTTATTGTTGAAACAGAAAGCAGAGCTGGCTAA
 TCCCAAGGCAGTG**TGA**CTCAGCTAACCAATGTCTCCAGGCTATGAAATTGGCGAT
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 TCGTGCTTATTGGATTGCAAAAGGGAGTCCCACCATCGCTGGTGGTATCCAGGGTCCCTG
 CTCAAGTTCTTGAAAAGGAGGGCTGGAATGGTACATCACATAGGCAAGTCCTGCCCTGT
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10015865
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FIGURE 8

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LTLEDYREPIEVNLFGlisVTLNMLPLVKKAQGRVINVSSVGGRLAIVGGGYTPSKYAVEGF
NDSSLRRDMKAFGVHVSCIEPGLFKTNLADPVKVIEKKLAIWEQLSPDIKQQYGEFYIEKSLD
KLKGNKSYVNMDLSPVVECMDHALTSLFPKTHYAAGKDAKIFWIPLSHMPAALQDFLLLKQK
AELANPKAV
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 136-152

N-glycosylation sites.

amino acids 161-163, 187-190 and 253-256

Glycosaminoglycan attachment site.

amino acids 39-42

N-myristoylation sites.

amino acids 36-41, 42-47, 108-113, 166-171, 198-203 and 207-212

FIGURE 9

GC GGGCTGTTGACGGCGCTGCG**A**TGGCTGCCTGCGAGGGCAGGAGAAGCGGAGCTCTCGGTT
 CCTCTCAGTCGGACTTCTGACGCCGAGTGGCGGGGCCCTGGGCCGTGCCACCACT
 GTAGTCATGTACCCACCGCCGCCGCCTCATCGGA~~CT~~TCATCTCGGTGACGCTGAG
 CTTGGCGAGAGCTATGACAACAGCAAGAGTTGGCGGCCGCTCGTGTGGAGGAATGGA
 AGCAACTGTGAGATTGCAGCGAATATGATTCTTCTCCTTGCTTCTGCTTTCTGT
 GGACTCCTCTACATCAACTGGCTGACCATTGAAAGCTCTGGCTTCAGGCTAGAGGA
 AGAGCAGAAGATGAGGCCAGAAATTGCTGGTTAAAACCAGCAAATCCACCCGTCTTACCAAG
 CTCCTCAGAAGGCCGACACCACCGTACAGACTTACCTGAGATTTCGTACAGAACACAA
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 CTCCCTCAAGAAGAGCAGAAGTCCCACCAAGCCTCCCTGCCACCGGCCAGGACACAGGG
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 GAGGAAAGAATTGAGGAAGCCAGGAAGTGGGTGTCGAAGAAGTTACACTTGAAAAGGACG
 TGGACGTCAACCTGTTGAGAGCACGATCCGCATCCTGGGGGGCTCCTGAGTGCCTACCAC
 CTGTCGGGACAGCCTCTCCTGAGGAAAGCTGAGGATTGGAAATCGGCTAATGCCTGC
 CTTCAAGAACACCACCAAGATTCTTACTCGGATGTGAACATCGGTACTGGAGTTGCCACC
 CGCCACGGTGGACCTCCGACAGCACTGTGGCGAGGTGACCCAGCATTAGCTGGAGTTCCGG
 GAGCTCTCCGTCTCACAGGGATAAGAAGTTCAAGGAGGCTGGTGCCTCATCAATACCCACAGCA
 CATCCACGGCTGTCTGGGAAGAAGGATGGCTGGTGCCTCATCAATACCCACAGTG
 GCCTCTCACCCACCTGGCGTATTACGCTGGCGCCAGGGCCACAGCTACTATGAGTAC
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 GCTCATGGAGACTTGT~~T~~ACAGATGAACCGCAGATGGAGACGGGCTGAGTCCCAGATCG
 TGCAC~~T~~CAACCTTACCCCGCCGGCGCTGGACGTGGAGGTCAAGCCAGCAGACAGG
 CACAACCTGCTGCCAGAGACCGTGGAGAGCCTGTTCTACCTG~~T~~ACCGCGTACAGGGGA
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 CCTCGGGTGGCTATTCTCATCAACATGTCCAGGATCCTCAGAAGCCCAGCCTAGGGAC
 AAGATGGAGAGCTTCTTCTGGGGAGACGCTCAAGTATCTGTTCTGCTCTCCGATGA
 CCCAACCTGCTCAGCCTGGACGCCTACGTGTTAACACCGAAGCCCACCCCTGCCTATCT
 GGACCCCTGCC**TAG**GGTGGATGGCTGTTGAGGGACTTCGGGTGGCAGAGGCACCTG
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 CTGGCCGCCCGCAGGGGCTGGAGGGCTGGACGGCAAGTCCGTAGCTCACGGCCCT
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1000153639 4241004

FIGURE 10

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><subunit 1 of 1, 699 aa, 1 stop
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IAGLKPANPPVLPAPQKADTDPENLPEISSQKTQRHIQRGPPHLQIRPPSQDLKDGTQEEAT
KRQEAPVDPREGDPPQRTVISWRGAVIEPEQGTELPSRRAEVPTKPLPPARTQGTPVHLNY
RQKGVIDVFLHAWKGYRKFAWGHDELKPVSRSFSEWFGLGLTLIDALDTMWILGLRKEFEEA
RKWVSKKLHFEKDVDVNLFESTIRILGGLLSAYHLSGDSLFLRKAEDFGNRLMPAFRTPSKI
PYSDVNIGTGVAHPPRWTSDSTVAEVTSIQLEFRELTSRLTGDKKFQEAVEKVTQHIHGLSGK
KDGLVPMFINTHSGLFTLGVFTL GARADSYYEYLLKQWIQGGKQETQLLEDYVEAIEGVRT
HLLRHSEPSKLT FVGELAHGRFSAKMDHLCFLPGTLALGVYHGLPASHMELAQELMETCYQ
MNRQMETGLSPEIVHFNLYPQPGRRDVEVKPADRHNL RPETVESLFYLYRVTGDRKYQDWG
WEILQSFSRFTRVPSGGYSSINNVQDPQKPEPRDKMESFFLGETLKYLFL FSDDPNLLSLD
AYVFNTEAHPLPIWTPA

Important features of the protein:

Transmembrane domain:

amino acids 21-40 and 84-105 (type II)

FIGURE 11

GGCGCCGCGTAGGCCCGGGAGGCCGGCCGGCCGGCTGCGAGCGCCTGCCCATGCGCCGC
 CGCCTCTCCGCACG**ATG**TTCCCTCGCGGAGGAAAGCGGCCAGCTGCCCTGGGAGGACGGC
 AGGTCCGGGTTGCTCTCCGGCGGCCCTCCCTCGGAAGTGTTCGTCTCACCTGTTCGTGGC
 CTGCCTCTCGCTGGCTTCTTCTCCACTCTGGCTGCAGCTCAGCTGCTCTGGGACGTGG
 CCCGGCAGTCAGGGACAAGGGCAGGAGACCTCGGCCCTCCCCGTGCCTGCCCTAGAG
 CCGCCCCCTGAGCACTGGAAAGAAGACGCATCCTGGGCCCCACCGCCTGGCAGTGCTGGT
 GCCCTCCGCGAACGCTTCGAGGGAGCTCCTGGTCTCGTCCCCACATGCGCCGCTCCTGA
 GCAGGAAGAAGATCCGGCACCATCTACGTGCTCAACCAGGTGGACCACCTCAGGTTAAC
 CGGGCAGCGCTCATAACGTGGCTTCTGGAGAGCAGCACAGCACGGACTACATTGCCAT
 GCACGACGTTGACCTGCTCCCTCTCAACGAGGAGCTGGACTATGGCTTCCTGAGGCTGGC
 CCTTCCACGTGGCCTCCCCGGAGCTCCACCCCTCTACCAACTACAAGACCTATGTCGGCGG
 ATCCTGCTGCTCTCCAAGCAGCACTACCGGCTGTGCAATGGATGTCCAACCGCTTCTGGG
 CTGGGCCGAGGACGAGTTCTACCGCGCATTAAGGGAGCTGGCTCCAGCTTCC
 GCCCTCGGAATACAACACTGGTACAAGACATTGCCACCTGCATGACCCAGCCTGGCG
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 AGGCCTGAACACTGTGAAGTACCATGTGGCTCCCGCACTGCCCTGTCGTGGCGGGGCC
 CCTGCACTGTCTAACATCATGTTGGACTGTGACAAGACGCCACACCCTGGTGCACATT
 AGC**TGA**GCTGGATGGACAGTGAGGAAGCCTGTACCTACAGGCCATTGCTCAGGCTCAGGA
 CAAGGCCTCAGGTCGTGGCCCAGCTCTGACAGGATGTGGAGTGGCCAGGACCAAGACAGCA
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 14241
 1000
 15265
 14241
 1000

FIGURE 12

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RHIIYVLNQVDHFRFNRNALINVGFLESSNSTDYIAMHDVDLLPLNEELDYGFPEAGPFHVA
SPELHPLYHYKTYVGGILLSKQHYRLCNGMSNRFWGWGREDDFYRRIKGAGLQLFRPSGI
TTGYKTFRHLHDPAWRKRDQKRIAAQKQEKFVDRREGGLNTVKYHVASRTALSVGGAPCTVL
NIMLDCDKTATPWCTFS
```

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 29-49 (type II)

N-glycosylation site.

amino acids 154-158

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 27-31

Tyrosine kinase phosphorylation site.

amino acids 226-233

N-myristoylation site.

amino acids 19-25, 65-71, 247-253, 285-291, 303-309, 304-310

FIGURE 13

CAATTTGCCTATCCACCTCCCCAAGCCCCCTTACCT**ATG**CTGCTGCTAACGCTGCTGCT
GCTGCTGCTGCTTAAAGGCTCATGCTGGAGTGGGACTGGTCGGTGCCCAGAAAGTCT
CTTCTGCCACTGACGCCCATCAGGGATTGGGCCTCTTCCCCCTCCTTGTGCTC
CTGCCTCATCGGCCTGCCATGACCTGCAGCCAAGCCCAGCCCCGTGGGAAGGGGAGAAAGT
GGGGGATGGC**TAA**GAAAGCTGGGAGATAGGGAACAGAACAGAGGGTAGTGGTGGCTAGGGGG
GCTGCCTATTAAAGTGGTGTATGATTCTTACTAATTATAACAAAGATATTAAGGC
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FIGURE 14

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PRGEGEKVGDG
```

Important features:

Signal peptide:

amino acids 1-15

Growth factor and cytokines receptors family:

amino acids 3-18

FIGURE 15

GGGACCCATGCGGCCGTGACCCCCGGCTCCCTAGAGGCCAGCGCAGCCGAGCGGACAAAG
 GAGCATGTCCCGCGCCGGGAAGGCCGTCCTCCGGCCATAAGGCTCCGGTGCCTGG
 GCCCGCGCCCGCTCCTGCCGCCGGCTCCGGGCCGCTAGGCCAGTGCCTGG
 CTCGCCCGCAGGCCGGCCGCAGC**ATG**GAGCCACCCGGACGCCGGCGGGCCGCGCA
 GCCGCCGCTGTTGCTGCCGCTCGCTGTTAGCGCTGCTCGCCTGCTGGGAGGCGGCG
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 GGCTAAACCTTCGGGAATTGTTTCTCATTATCTCAAGGAACCTTGATTATCTGCG
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 GCATCGCTGGTAAAGGAGAAGAACATCACGGTACGGGATACCAGGTGTGTTATCCTAAGT
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 GGAGAAATAGTGAAACCGATGAATCGCAAGGTATTTGTTGAAAAGAACATGATTCAAAC
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 TGCATAATAACTGATCCAACAGGTGTTAGGTGTTAGTGTGAGCACTCAATAAATA
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1 0 0 1 5 3 6 9 1 4 3 1 4 0 1

FIGURE 16

MEPPGRRRGRAQPPLLPLSLLALLALLGGGGGGAAALPAGCKHDGRPRGAGRAAGAAEGK
 VVCSSLELAQVLPPDTLPNRTVTLLISNNKISELKNGSFSGSLLERLDLRNNLISSIDPGAFWGLSSLKRLLDLTNNRIGCLNADIFRGLTNLVRNLSGNLFSSLSQGTFDYLASLRSLEFQTEYLLCDCNILWMHRWVKEKNITVRDTRCVYPKSLQAQPVTGVKQELLTCDPPLPELFYMTPSHRQVVFEGDSLFPQCMASYIDQDMQVLWYQDGRIVETDESQGIFVEKNMIHNCSLIASALTISNIQAGSTGNWGCHVQTKRGNNTRTVDIVVLESSAQYCPPERVVNNKGDFRPRTLAGITA
 YLQCTRNTHGSIGYPGNPQDERKAWRRCDRGGFWADDYSRCQYANDVTRVLYMFNQMPLNL
 TNAVATARQLLAYTVEAANFSDKMDVIFVAEMIEKFGRFTKEEKSKELGDVMDIASNIMLA
 DERVLWLAQREAKACSRIVQCLQRIATYRLAGGAHVYSTYSPNIALEAYVIKSTGFTGMTCT
 VFQKVAASDRTGLSDYGRRDPEGNLDKQLSFKCNCNSNTFSSLALKVCYILQSFKTIYS

Signal peptide:

amino acids 1-33

Transmembrane domain:

amino acids 13-40 (type II)

N-glycosylation site.

amino acids 81-85, 98-102, 159-163, 206-210, 301-305, 332-336, 433-437, 453-457, 592-596

N-myristoylation site.

amino acids 29-35, 30-36, 31-37, 32-38, 33-39, 34-40, 51-57, 57-63, 99-105, 123-129, 142-148, 162-168, 317-323, 320-326, 384-390, 403-409, 554-560

FIGURE 17

GC GTGGGGATGTCTAGGAGCTCGAAGGTGGTGCTGGGCCTCTCGGTGCTGCTGACGGCGGCC
ACAGTGGCCGGCGTACATGTGAAGCAGCAGTGGGACCAGCAGAGGCTTCGTGACGGAGTTAT
CAGAGACATTGAGAGGCAAATTGGAAAAAGAAAACATTCGTCTTTGGGAGAACAGATTA
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TCATGACTTGAATGTGAAATATCTGTTGGACAGACAACACGAGTTGTGTGTGTTGAT
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AATAAAGGACAGTGGTCATATAAGTTACTGCTTCAGGGTCCCTTATATCTGAATAAAGGA
GTGTGGGCAGACACTTTGGAAAGAGTCTGTCTGGGTGATCCTGGTAGAAGCCCCATTAGGG
TCACTGTCCAGTGCTTAGGGTTTTACTGAGAACACTGCCAGCTGTGAGAAGGAAGGG
TGGATAGTAGCATCCACCTGAGTAGTCTGATCAGTCGGCATGATGACGAAGCCACGAGAAC
TCGACCTCAGAAGGACTGGAGGAAGGTGAAGTGGAGGGAGAGACGCTCCTGATCGTCGAATCC

FIGURE 18

MSRSSKVVLGLSVLLTAATVAGVHVVKQQWDQQQLRDGVIRDIERQIRKKENIRLLGEQIILT
EQLEAEREKMLLAKGSQKS

Signal peptide:

amino acids 1-21

FIGURE 19

CTGTCGTCTTGCTTCAGCCGCAGTCGCCACTGGCTGCCTGAGGTGCTCTTACAGCCTGTT
 CAAGTGTGGCTTAATCGTCTCCACCACCAGATCTTCTCCGTGGATTCTGCTAAGACC
 GCTGCCATGCCAGTGACGGTAACCCGCACCACCATACAACCACGACGTCATCTCGGG
 CCTGGGGTCCCCATGATCGTGGGTCCCCTCGGGCCCTGACACAGCCCCTGGGTCTCCTCGC
 CTGCTGCAGCTGGTGTCTACCTGCGTGGCCTCTCGCTGGTGGTAGCGTGGCGCTGGAC
 GGGTCCATGGCAACTGGTCCATGTTACCTGGTGCTTCTGCTTCCGTGACCGTGA
 TCCTCATCGTGGAGCTGTGCGGGCTCCAGGCCGCTTCCCCCTGTCTGGCGCAACTCCCC
 ATCACCTTCGCCTGCTATGCGGCCCTCTCTGCCTCTCGGCCATCATCTACCCACAC
 CTATGTCCAGTCCCTGCCCACGGCGTTCGCGGGACCACGCCATGCCGCCACCTTCTT
 CCTGCATCGCGTGTGGCTTACGCCACCGAACCGTACCCGGCTGCTGAAGGTGCTGGAGAC
 ATCACTGGCTATATGGCCACCGTACCCGGCTGCTGAAGGTGCTGGAGACCTCGTTGCCTG
 CATCATCTCGCGTTCATCAGCGACCCAACCTGTACCAAGCACCAGCCGGCCCTGGAGTGG
 GCGTGGCGGTGTACGCCATCTGCTTACCTAGCGGCCATGCCATCCTGCTGAACCTGGGG
 GAGTGCACCAACGTGCTACCCATCCCCTCCCCAGCTTCTGTCGGGGCTGGCCTGCTGTC
 TGTCCCTCTATGCCACCGGCCCTGTTCTGCCCCCTCTACCAGTTGATGAGAAAGTATG
 GCGCCAGCCTCGCGCTCGAGAGATGTAAGCTGCAGCCGAGCCATGCCACTACGTGTGT
 GCCTGGGACCGCCACTGGCTGTGGCCATCCTGACGCCATCAACCTACTGGCGTATGTGGC
 TGACCTGGTGCACTCTGCCAACCTGGTTTGTCAAGGTCTAAGACTCTCCAAGAGGCTCC
 CGTTCCCTCTCCAACCTTTGTTCTTGCACCGAGTTCTTATGGAGTACTTCTTCC
 TCCGCCCTTCCTCTGTTCTTCTTCCCTGTCTCCCTCCACCTTTCTTCCCT
 CAATTCCCTGCACTCTAACCAAGCTTGATGCATCTTCTTCCCTTCCCTTGT
 TTCCTCTGTGTTGTTGTTGCCACATCCTGTTTCAACCCCTGAGCTGTTCTTCTT
 CTTTCTTCTTTTTTTTTTTAAGACGGATTCTCACTCTGTCGGCCAGGCTGGAG
 TGCAGTGGTGCATCTCAGCTACTGCAACCCCCGCCTGGGTTCAAGCGATTCTCCTCC
 CCCAGCCTCCAAAGTAGCTGGGAGGACAGGTGTGAGCTGCCGCACCCAGCCTGTTCTT
 TTCCACTCTTCTTTCTCATCTTCTGGGTTGCCTGTCGGCTTCTTATCTGCCGT
 TTTGCAAGCACCTCTCCTGTGTCCTGGGAGCCCTGAGACTTCTTCTCCTGCCCTCA
 CCCACCTCCAAGGTGCTGAGCTCACATCCACACCCCTGCAGCGTCCATGCCACAGCCCC
 CCAAGGGGCCATTGCCAAAGCATGCCCTGCCACCCCTGCTGTGCCTTAGTCAGTGTAC
 GTGTGTGTGTGTGTTGGGGGGTGGGGGGTAGCTGGGATTGGGCCCTTTCT
 CCCAGTGGAGGAAGGTGTGAGCTACTTCCCTTAAATTAAAAACATATATATATAT
 ATTTGGAGGTCACTTCAATGGCGGGAGGCATTAAGCACCGACCCCTGGTCCCTAGG
 CCCCGCCTGGCACTCAGCCTGCCAGAGATTGGCTCCAGAATTGGCAGGCTACAGAACAC
 CCACTGCCTAGAGGCCATCTTAAAGGAAGCAGGGCTGGATGCCCTTACCCAACTATTCT
 CTGTGGTATGAAAAAG

FIGURE 20

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58727
<subunit 1 of 1, 322 aa, 1 stop
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SMGNWSMFTWCFCFSVTLIIILIVELCGLQARFPLSWRNFPITFACYAALFCLSASIIYPTTY
VQFLSHGRSRDHAIATFFSCIACVAYATEVAWTRARPGEITGYMATVPGLLKVLTFVACI
IFAFISDPNLYQHQPALEWCVAVYAICFILAAIAILLNLGECTNVLPPIPFPSSLGALLSV
LLYATALVLWPLYQFDEKYGGQPRRSRDVSCSRSHAYYVCAWDRRILAVAILTAINLLAYVAD
LVHSAHLVFKV
```

Important features:

Transmembrane domains:

amino acids 41-60 (type II), 66-85, 101-120, 137-153, 171-192,
205-226, 235-255 and 294-312

N-glycosylation site.

amino acids 66-69

Glycosaminoglycan attachment site.

amino acids 18-21

FIGURE 21

GAACGTGCCACCAGCCCAGCTAATTTGTATTTAGTAGAGACGGGGTTTCAACCAGTGGCCAGGCTGGTC
 TTGAACTCGTGACCTCATGATCGCTCACCTCGGCCTCCAAAGTGCTGGATTACAGGCATGAGCCACTGACGC
 CTGGCAGCCTATGCATTAAAGAAATTATTCTGTATTAGGTGCTGTGCTAAACATTGGGACTACAGTGACCA
 AACAGACTGAATTCCCCAAGAGCAAAGACAGTGAGGGAGACCAACAAGAAACAGGAATGCAAAAGAGACCA
 TTATTACTCACTATGACTAAGGTACAATGGGTACGTTGATGGAGAGTGATTGTTAAGAGACTACAGAGGG
 AGGACAGACTACCAAGAGGGGCCAGGAAAGCTCCTCTGACGAGGTGGTATTCAGGCCAAACTGGAAGAATGA
 GAAAGAGCTAGCCAGGCCATCAGAATAGTCCAGAAGAGATGGGAGCACTACACTACACTACACTTTGGCCTGAGAA
 AATAGCATGGGATTGGAGGAGCTGGGGAACACCAACTTCTGCCGACCTGGCAGGAGGCATTGAGGGCTTGAGA
 AAGGGCAATGGCAGTAGCAGTAGAAAGGACAGGGTAGGAGCAGGGACTTGCAGGTGGAATCATTAGGTCTTATC
 AACAGATATGGGCAAGCAAAGCCAGGGAGAATTGATGTTAATGCTGAGGTTGGAGCCAGGGTAGATGGGACAG
 TGGTGGGTGATGCAAAGGAAAGAGGTAGGAAGCAGGGCCAGCAGTGGGAGAAGGTGTGGGGTTGGTTCCA
 TCTTGGCAGTCTGCCGAATGTGGATGGGAAGACCAAGAGGAGGAGCAAGGGGAGAGGGGAAGGGAAATCTTAA
 AGAAGTCCTGGATGCCACACTCTTCTCTCTCTCTCTCAGAGTCTCACTCGTGGTTCTTACAGGTTCTTATC
 TTCCTGCCCTGCCCTCATCTCCTCTGGGTGCTGGAAAGTGGAGGATTAGCTGAAGTTGCTTCTCGGGGCTG
 TCTGAATCTCATTGCTTCTGGGAGGACATAATTACACCTGTCCTAGCTTCTTATCATCTTACATTCCCTGTAG
 CCACTGGGACATATGTTGCTCTCTAGCTCTGTCTCTCTCATGCCCTTGCTGGGTATGGCATGTTAG
 GGGGAAGGTATTGCTGCAAGGGGCACTGACTTTCTAATGGTGTACCCAAGGTGAATGTTGGAGACACAGTC
 GCGATGCTGCCCAAGTCCCCGGAGGCCCTAACTATCCAGGAGATCGCTGCGCTGGCAGGTCTCCCTGCATGGT
 ATGCAGCCCCCTCCCATGTTCTGGCCACTTGTCTTCTCTCCGTTGCACATCCCTTGGAACTGTTCT
 GTGAGTACATGCTGGGTCTCCCCCTTCTTCCCTGCTCAGGTGAATCTCAGCCCCCTCTCCACCCAAAGGTTC
 ACATGGATCTAACTACTGCCACCCCTTCCACCTCCCTGCACCTGTGCTCCCTGGCCTGGCTTACCAAGGGCTTC
 TCCACCCCTCCCTATCTCCAGGTATTTCCAGGTGGTGAAGGGACACGTGACCAAGCCTACCCCATGGCCCAGG
 GCCGAGTGGCTCACCTCATTGAGTGGAAAGGGCTGGAGCAAGCGAGTGAACCTGCTGCCCTGGAATCAGCCT
 TTTCCCTTATTGACACTCAGCAGGGGAACAAAGAGGCTCGCTTGCAGGAGTGGCTGACCTGGAGCTTGGCA
 TCGCGGAAGCCAAGCTCCGAGCATGGTCTTGGTGGATGGCAGGACTCCACTGATGACTCCTATGATGAGGACT
 TTGCTGGGGAAATGGACACAGACATGGCTGGCAGCTGCCCTGGGCCACCTCCAGGACCTGTTCACCGGGCC
 ACCGGTTCTCCGGCCTGTGCGCCAGGGCTCGTGGAGCCTGAGAGCGACTGCTCACAGACCGTGTCCCCAGACA
 CCCGTGCTCTAGTCTGTGAGCCTGGAGGATGGTGTGGCTCCCGGCCGCTGGCTCCAGCTGCTGG
 GCGATGAGCTGCTCTGCCAAACTGCCCGGGAAAGTGCCTTCCGAGCCTGGGCCACTGGAGGCCCC
 AGGACTCACTCTACAACCTGCCCTCACAGAGTCTGCCTTCCCCCGGGAGGAGGAGGCCAGCCCCCTGCAAGG
 ACTGCCAGCCACTCTGCCACCACTAACGGGCAGTGGAACGGCAGGGCAAGCCTGACCTGGCTCT
 GGGTGGTGTCTTAGATGAGGATGAGGCAGAGCAGAGGAACAGTGAACCCACATCATGCCCTGGCAGTGGCATGCA
 TCCCCCGCTGCTGCCAGGGCAGAGCCTCTGTGCCCAAGTGTGGCTCAAGGCTCCAGCAGAGCTCCACAGCC
 TAGAGGGCTCTGGAGCGCTCGCTTCTCGTTGTGTTTGATGAAAGTGTGGAGAGGAGGAGGGCTG
 GGCTGGGGCGCATGTCCTGCCCTACTCCGGGCTTGCGGGGGCTGCCCCGGGCTCTGGGCATGGCTACA
 GCTGTGGCAGACAGTGATGTTCATGTTCTAAATGCCACACACATTCTCTCGGATAATGTGAACCACTA
 AGGGGGTTGTGACTGGGCTGTGAGGGTGGGGAGGGGCCAGCAACCCCCCACCCTCCCCATGCTCTC
 TCTTCTGCTTTCTCTCACTTCCGAGTCCATGTGAGTGCTGCTTGATAGAATCACCCCCCACCTGGAGGGCTGG
 CTCTGCCCTCCGGCCTATGGGTGAGCGCTCCCTCAAGGGCCCTGCCCAGCTGGCTGTGCTGTGCTTC
 ATTACACCTCTCCATCGTCTCTAAATCTCTCTTCTAAAGACAGAAGGTTTTGGTCTGTTCTCAGTC
 GGATCTCTCTCTGGGAGGCTTGGAAATGATGAAAGCATGTACCCCTCCACCTTCTGGCCCTTAATGG
 GGCCTGGGCCCTTCCCAACCCCTCCTAGGATGTGCGGGCAGTGTGCTGGCCTCACAGCCAGCCGGGCTGCC
 ATTCAAGCAGAGCTCTGAGCGGGAGGTGAAAGAAAGGATGGCTCTGGTGCCACAGAGCTGGGACTTCATGTT
 CTTCTAGAGAGGGCCACAAGAGGGCCACAGGGTGGCGGGAGTTGTCAGCTGATGCCCTGCTGAGAGGCAGGAAT
 TGTGCCAGTGAAGTGAACAGTCATGAGGGAGTGTCTTCTGGGAGGAAAGAAGGTAGAGCCTTCTGCTGAAT
 GAAAGGCCAAGGCTACAGTACAGGGCCCGCCCCAGCCAGGGTGTAAATGCCACAGTGTGGAGGCTCTGGCAG
 ATCCTGCATTCCAAGGTCACTGGACTGTACGTTTATGGTGTGGGAAGGGTGGGTGGCTTAAAGAATTAGGC
 CTTGTAGGCTTGGCAGGTAAGAGGGCCAAGGTAAGAACAGAGGCCAACGGCACAAGCATTCTATATAAGT
 GGCTCATTAGGTGTTATTTGTTCTATTAAAGAATTGTTTATTAAATTAAATAAAAATCTTGTAAATCTC
 TAAAAA

FIGURE 22

MFLATLSFLLPFAHPFGTVSCEYMLGSPLSSLAQVNLSPESHPKVHMDPNYCHPSTSLHLCS
LAWSFTRLLHPPLSPGISQVVKDHTKPTAMAQGRVAHLIEWKGWSKPSDSPAALSAFSSY
SDLSEGEQEAFRAAGVAEQFAIAEAKLRAWSSVDGEDSTD SYDEDFAGGMDTDMAGQLPLG
PHLQDLFTGHRFSRPVRQGSVEPESDCSQTVPDTLCSSLCSLEDGLLGSPARLASQLLGDE
LLLAKLPPSRESAFRSLGPLEAQDSLYNSPLTESCLSPAEEEPAPCKDCQPLCPLTGWER
QRQASDLASSGVVSLDEDEAEPEEQ

Signal peptide:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 123-127, 128-132, 155-159, 162-166, 166-170, 228-232,
285-289, 324-328

Tyrosine kinase phosphorylation site.

amino acids 44-52

N-myristoylation site.

amino acids 17-23, 26-32, 173-179

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 11-22

FIGURE 23

GGTCTCTGGCGCTCTGTTACACAAGCAAGATAACAGCCAGCCCCACCTAATTGTTTCCCT
GGCACCCCTCCTGCTCAGTGCGACATTGTCACACTTAACCCATCTGTTTCTCTAATGCACGA
CAGATTCCTTCAGACAGGACAACGTGATATTCAGTTCTGATTGAAATACCTCCAAG
CCTGAAGCTCTGTTACTAGCCATTGTGAGCTCAGTTCTCATCTGAAAATGGGCATAA
TACAATCTATTCTGCCACATCAAGGGATTGTTATTCTTTAAAAAAACCAATACCAAAG
AAGCCTACAATGTTGGCCTAGCCAAAATTCTGTTGATTCAACGTTGTTTATTCACTTCT
ATCGGGGAGCCATGGAAAAGAAAATCAAGACATAAACACAACAGAACATTGCAGAAGTT
TTAAAACAATGGAAAATAACCTATTCTTGAAAGTGAAGCAAACCTAAACTCAGATAAA
GAAAATATAACCACCTCAAATCTCAAGGCGAGTCATTCCCCTCTGAATCTACCCAAACAA
CAGCCACGGAATAACAGATTCTCCAGTAACACTCATCAGCAGAGCATTCTGGCAGTCTAA
AACCCACATCTACCATTCCACAAGCCCTCCCTGATCCATAGCTTGTTCTAAAGTGCCT
TGGAAATGCACCTATAGCAGATGAAGATCTTGCCCCTCAGCACATCCAAATGCTACACC
TGCTCTGTCTTCAGAAAACCTCAGTGGCTTGGTCAATGACACCGTGAAAACCTCTGATA
ACAGTCCATTACAGTTAGCATTCTCTCTCAGAACCAACTTCTCCATCTGTGACCCCCCTG
ATAGTGGAACCAAGTGGATGGCTTACCAACAAACAGTGAAGTAGCTTCACTGGGTTACCCCTTA
TCAAGAAAAAAACAACCTACAGCCTACCTAAAATTACCAATAATTCAAACCTTTCCAA
ATACGTCAAGATCCCCAAAAGAAAATAGAAATACAGGAATAGTATTGGGCCATTAGGT
GCTATTCTGGGTGTCATTGTTACTCTTGTGGCTACTTGTGTGGAAAAAGGAAAAC
GGATTCTTCCATCGGCGACTTATGACGACAGAAATGAACCAGTCTCGGATTAGACA
ATGCACCGAACCTTATGATGTGAGTTGGATTCTAGCTACTACAATCCAACCTTGAAT
GATTGCCATGCCAGAAAGTGAAGAAAATGCACGTGATGGCATTCTATGGATGACATACC
TCCACTTCGTACTCTGTATAGAACAAACAGAAAAAGGCGTTAACAGCAAGTGTCTA
CATCCTAGCCTTGTACAAATTCTTCAAAAGGTTACACAAATTACTGTCACGTGGAT
TTTGTCAAGGAGAATCATAAAAGCAGGAGACCAGTAGCAGAAATGTAGACAGGATGTATCAT
CCAAAGGTTCTTCTTACAATTGGCCATCCTGAGGCATTACTAACAGTACGCCCTTAATT
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TCACCATTACAGCCCTGCCCTACATAACTAAATAAAAAATTATTCCACCAAAAAATTCTAAA
ACAATGAAGATGACTCTTACTGCTCTGCCAGGCCCTAGTACCAATTCAAGATTGCAT
TTCTTAAATGAAAATTGAAAGGGTGTGTTAAAGAAAATTGACTTAAAGCTAAAAGAG
GACATAGCCCAGAGTTCTGTTATTGGAAATTGAGGCAATAGAAAATGACAGACCTGTATT
TAGTACGTTATAATTCTAGATCAGCACACATGATCAGGCCACTGAGTTATGAAGCTGA
CAATGACTGCATTCAACGGGCCATGGCAGGAAAGCTGACCCCTACCCAGGAAAGTAATAGCT
TCTTAAAGTCTCAAAGGTTGGAAATTAACTTGTCTTAATATATCTTAGGCTTCAA
TTATTGGGTGCCTAAAAACTCAATGAGAATCATGGT

FIGURE 24

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58732
><subunit 1 of 1, 334 aa, 1 stop
><MW: 36294, pI: 4.98, NX(S/T): 13
MLALAKILLISTLFYSSLGSHGKENQDINTTQNIAEVFKTMENKPISLESEANLNSDKENI
TTSNLKASHSPPLNLPNNSHGITDFSSNSSAEHSLGSLKPTSTISTSPPPLIHSFVSKVPWNA
PIADEDILLPISAHPNATPALSSENFTWSLVNDTVKTPDNSSITVSILSSEPTSPSVTPLIVE
PSGWLTTSDFSFTGFTPYQEKTTLQPTLKFTNNSKLFPNTSDPQKENRNTGIVFGAILGAIL
GVSLTLVGYLLCGKRKTDSFSHRRLYDDRNEPVLRLDNAPEPYDVSFGNSSYYNPTLNSA
MPESEENARDGIPMDDIPPLRTSV

Signal peptide:

amino acids 1-23

Transmembrane domain:

amino acids 235-262

N-glycosylation site.

amino acids 30-34, 61-65, 79-83, 90-94, 148-152, 155-159,
163-167, 218-222, 225-229, 298-302, 307-311

FIGURE 25

AACAGGATCTCCTCTGCAGTCTGCAGCCCAGGACGCTGATTCCAGCAGCGCCTACCGCGC
 AGCCCGAAGATTCACT**ATG**GTAAAATCGCCTCAATAACCCCTACCGCCGTGCAAAAGGAGG
 AGGCCGGCAAGACGTGGAGGCCCTCCTGAGCCGCACGGTCAGAACTCAGATACTGACCGGC
 AAGGAGCTCCGAGTTGCCACCCAGGAAAAAGAGGGCTCCTCTGGGAGATGTATGCTTACTCT
 CTTAGGCCTTCATTCATCTTGGCAGGACTTATTGTTGGAGCCTGCATTACAAGTACT
 TCATGCCAAGAGCACCATTACCGTGGAGAGATGTGCTTTGATTCTGAGGATCCTGCA
 AATTCCCTCGTGGAGGAGAGCCTAACCTCCTGCCTGTGACTGAGGAGGCTGACATTGTGA
 GGATGACAACATTGCAATCATTGATGTGCCTGTCCCCAGTTCTGTGATAGTGACCCCTGAG
 CAATTATTGACTTTGAAAAGGGAAATGACTGCTTACCTGGACTTGTGCTGGGAACACTGC
 TATCTGATGCCCTCAATACTTCTATTGTTATGCCTCCAAAAAATCTGGTAGAGCTCTTGG
 CAAACTGGCGAGTGGCAGATATCTGCCTCAAACCTATGTGGTTCGAGAAGACCTAGTTGCTG
 TGGAGGAAATTGATGTTAGTAACCTGGCATCTTATTACCAACTTGCAATAACAGA
 AAGTCCTCCGCCTCGCGAGACCTCTGCTGGTTCAACAAACGTGCCATTGATAA
 ATGCTGGAAGATTAGACACTTCCCCAACGAATTATTGTTGAGACCAAGATCTGTCAAGAG**T**
AAGAGGCAACAGATAGAGTGTCTGGTAATAAGAAGTCAGAGATTACAATATGACTTTAA
 CATTAAGGTTATGGGAACTCAAGATATTACTCATGCATTACTCTATTGCTTATGCTTT
 AAAAAAAGGAAAAAAAAAAACTACTAACCAACTGCAAGCTTGTCAAATTAGTTAAT
 TGGCATTGCTGTTTTGAAACTGAAATTACATGAGTTTCATTTCCTTGCAATTAG
 GTTTAGATTCTGAAAGCAGCATGAATATATCACCTAACATCCTGACAATAATTCCATCC
 GTGTTTTTTGTTGTTGTTCTTTCTTAAGTAAGCTCTTATTGATCTTATGCTTATG
 GTGGAGCAATTAAAATTGAAATATTAAATTGTTTGAACCTTTGTAAATTATA
 TCAGATCTAACATTGTTGGTTCTTTGTTTCAATTGTACAACCTTCTGAATTAGA
 AATTACATCTTGCAGTTCTGTAGGTGCTCTGTAATTAAACCTGACTTATATGTAAATT
 TTCATGAGACAGTCATTAACTAATGCAGTGATTCTTCTCACTACTATCTGTATTGTGG
 AATGCACAAAATTGTGTAGGTGCTGAATGCTGTAAGGAGTTAGGTGTATGAATTCTACAA
 CCCTATAATAAAATTACTCTATACAAAAA

FIGURE 26

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58828
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ILAGLIVGGACIYKYFMPKSTIYRGEMCFDSEDPANSLRGGEPNFLPVTEEADIREDDNIA
IIDVPVPSFSDSDPAAIHDFEKGMTAYLDLLLGNCYLMPPLNTSIVMPPKNLVELFGKLASG
RYLPQTYVVREDLVAVEEIRDVSNLGIFTYQLCNNRKSFRLRRRDLLLGFNKRAIDKCWKIR
HFPNEFIVETKICQE
```

Type II transmembrane domain:

amino acids 53-75

N-glycosylation site.

amino acids 166-170

Casein kinase II phosphorylation site.

amino acids 35-39, 132-136, 134-138

N-myristoylation site.

amino acids 66-72, 103-109

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 63-74

FIGURE 27

GGAGGAGGGAGGGCGGGCAGGCAGCCAGAGCAGCCCCGGGCACCAGCACGGACTCTCT
 CTTCCAGCCCAGGTGCCCTTCACTCTCGCTCCATTGGCGGGAGCACCCAGTCCTGTACGCC
 AAGGAACCTGGCCTGGGGCACCATGTTTCGGCGGCAGCCCCAGCCTCCTCATCCTCTG
 TTGCTGCTGCTGGGTCTGTGCCTGCTACCGACGCCGCTCTGTGCCCTGAAGGCCACGTT
 CCTGGAGGATGTGGCGGGTAGTGGGGAGGCCGAGGGCTCGTCGGCCTCCTCCCCGAGCCTCC
 CGCCACCCCTGGACCCCGGCCCTCAGCCCCACATCGATGGGGCCCCAGCCCACAACCCTGGGG
 GGCCCATCACCCCCCACCACCTCCTGGATGGATAGTGGACTTCTCCGCCAGTACGTGAT
 GCTGATTGCTGTGGTGGCTCCCTGGCCTTCTGCTGATGTTCATCGTCTGTGCCCGGTCA
 TCACCCGGCAGAACAGAAGGCCCTGGCCTATTACCCATCGTCTTCCCCAAGAACAGTAC
 GTGGACCAAGAGTGACCGGGCCGGGGCCCCGGGCCTTCAGTGAGGTCCCCGACAGAGCC
 CGACAGCAGGCCCGAGGAAGCCCTGGATTCCCTCCGGCAGCTCCAGGCCGACATCTTGGCG
 CCACCCAGAACCTCAAGTCCCCACCAGGGCTGCACTGGCGGTGGGACGGAGCCAGGATG
 GTGGAGGGCAGGGCGCAGAGGAAGAGGAGAACGGCAGGCCAGGAGGGGACCAGGAAGTCCA
 GGGACATGGGGTCCCAGTGGAGACACCAGAGGCCGAGGAGGCCGTCAGGGGTCTTG
 AGGGGCTGTGGTGGCCGGTGAGGGCAAGGGAGCTGGAAGGGTCTCTTGTAGCCCAG
 GAAGCCCAGGGACCAGTGGTCCCCCGAAAGCCCTGTGCTGCAGCAGTGTCCACCCAG
 TGTCTAACAGTCCTCCGGCTGCCAGCCCTGACTGCTTCTGACACTCCCTCCTGGCCTCC
 GTGTATGAAAAGGCCTTCAGCCCTGACTGCTTCTGACACTCCCTCCTGGCCTCC
 TGCCAATCCCAGCATGTGCTGATTCTACAGCAGGCAGAAATGCTGGTCCCCGGTGCCCC
 GGAATCTTACCAAGTGCCATCATCCTCACCTCAGCAGCCCCAAAGGGCTACATCCTACAGC
 ACAGCTCCCTGACAAAGTGAGGGAGGGCACGTGTCCTGTGACAGCCAGGATAAAACATCC
 CCCAAAGTGCTGGATTACAGGCAGGCCACCGTGCCCGGCCAAACTACTTTTAAACA
 GCTACAGGGTAAAATCCTGCAGCACCCACTCTGGAAAATACTGCTCTTAATTTC
 TGAAGG
 TGGCCCCCTGTTCTAGTTGGTCCAGGATTAGGGATGTGGGTATAGGCATTAAATCCTC
 TCAAGCGCTCTCCAAGCACCCCCGGCCTGGGGTGAGTTCTCATCCGCTACTGCTGCTGG
 GATCAGGGTGAATGAATGGAACCTTCCTGTCTGGCCTCAAAGCAGCCTAGAACAGTGA
 GGG
 GCTGTGTTGAGGGACCTCCACCCCTGGGAAGTCCGAGGGCTGGGAAGGGTTCTGACG
 CCCAGCCTGGAGCAGGGGGCCCTGGCCACCCCTGTTGCTCACACATTGCTGGCAGCCTG
 TGTCACAATATTGTCAGTCCTCGACAGGGAGCCTGGCTCCGTCTGTTAGGGAGGCT
 CTGGCAGGAGGTCTCCCCCATCCCTCATCTGGGCTCCCCAACCTCTGCACAGCTCT
 CCAGGTGCTGAGATATAATGCACCAGCACAATAACCTTATTCCGGCCTGAAAAAAA
 AAAAAA
 AAAAAAAGA

1
 0
 0
 0
 1
 5
 8
 6
 5
 1
 4
 4
 0
 1
 0

FIGURE 28

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA58852
><subunit 1 of 1, 283 aa, 1 stop
><MW: 29191, pI: 4.52, NX(S/T): 0
MVSAAAPSLLLLLLLGSVPATDARSVPLKATFLEDVAGSGEAEGSSASSPSLPPPWTPAL
SPTSMGPQPTTLGGPSPTNFLDGIVDFRQYVMLIAAVGSLAFLLMFIVCAAVITRQKQKA
SAYYPSSFPKKYVDQSDRAGGPRAFSEVPDRAPDSRPEEALDSSRQLQADILAATQNLKSP
TRAALGGGDGARMVEGRGAEEEEEKSQEGDQEVTQGHGPVETPEAQEEPCSGVLEGAVVAGE
GQGELEGSLLLQAQEAQGPVGPPEPSPCACSSVHPSV
```

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 94-118

N-myristoylation site.

amino acids 18-24, 40-46, 46-52, 145-151, 192-198, 193-199,
211-217, 238-244, 242-248

FIGURE 29

GTGGACTCTGAGAAGCCCAGGCAGTTGAGGAAGGACAGGGAGAGAGAAGGCTGCAGACCCAGAGGGA
 GGGAGGAAGGGAGTCGGAAAGGAGGAGGACAGAGGAGGGCACAGAGACGCAGAGCAAGGGCG
 GCAAGGAGGAAGACCCTGGTGGGAGGAAGACACTCTGGAGAGAGAGGGGGCTGGCAGAG**ATG**
 AAGTTCCAGGGGCCCTGGCCTGCCTGCTGGCCCTCTGCCTGGCAGTGGGAGGGCTGG
 CCCCCCTGCAGAGCGGAGAGGAAAGCACTGGACAAATATTGGGAGGCCCTGGACATGGCC
 TGGGAGACGCCCTGAGCGAAGGGTGGAAAGGCCATTGGCAAAGAGGCCGGAGGGCAGCT
 GGCTCTAAAGTCAGTGAGGCCCTGGCCAAGGGACAGAGAAGCAGTTGGCACTGGAGTCAG
 GCAGGTTCCAGGCTTGGCGCAGCAGATGCTTGGCAACAGGGTCGGGAAGCAGCCCAG
 CTCTGGAAACACTGGCACGAGATTGGCAGACAGGCAGAACAGATGTCATTGACACGGAGCA
 GATGCTGTCCCGGCTCCTGGCAGGGGTGCCTGCCACAGTGGTCTGGAAACTCTGG
 AGGCCATGGCATCTTGGCTCTCAAGGTGGCCTGGAGGCCAGGGCAATCCTGGAG
 GTCTGGGACTCCGTGGTCCACGGATAACCCGGAAACTCAGCAGGCAGCTTGGAAATGAAT
 CCTCAGGGAGCTCCCTGGGTCAAGGAGGCAATGGAGGGCACCAAACCTTGGACCAACAC
 TCAGGGAGCTGTGGCCCAGCCTGGCTATGGTCAGTGAGAGCCAGCAACCAGAACATGAAGGGT
 GCACGAATCCCCCACCCTGGCTCAGGTGGAGGCTCCAGCAACTCTGGGGAGGCAGCGGC
 TCACAGTCGGCAGCAGTGGCAGCAGTGGCAGCAGCAGTGGCGGCAGCAGTGGCGGCAGCAGTG
 TGGCAGCAGTGGCAACAGTGGTGGCAGCAGAGGTGACAGCGGCAGTGAGTCCTCTGGGA
 TCCAGCACCGGCTCCTCCGGCAACCACGGTGGAGCGCGGGAGGAAATGGACATAAAC
 CGGGTGTAAAAGCCAGGGAATGAAGCCCGGGAGCGGGAAATCTGGATTAGGGCTTCA
 GAGGACAGGGAGTTCCAGCAACATGAGGAAATAAGCAAAGAGGCAATGCCCTTGG
 GGCTCTGGAGACAATTATCGGGGCAAGGGTCAGCTGGGCAGTGGAGGAGGTGACGCTGT
 TGGTGGAGTCATACTGTGAACCTGAGACGTCTGGATGTTAACTTGACACTTCT
 GGAAGAATTAAATCCAAGCTGGTTCATCAACTGGATGCCATAACAAAGGACAGAGA
 AGCTCTCGCATCCCG**TGA**CCTCCAGACAAGGAGCCACCAGATTGGATGGAGCCCCACACT
 CCCTCCTAAAAACACCACCCCTCTCATCACTAATCTCAGGCCCTGCCCTGAAATAACCTTA
 GCTGCCCAACAA
 AAA

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31

FIGURE 30

```

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59212
><subunit 1 of 1, 440 aa, 1 stop
><MW: 42208, pI: 6.36, NX(S/T): 1
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AGSKVSEALGQGTREAVGTGVRQVPGFGAADALGNRVGEAAHALGNTGHEIGRQAEDVIRHG
ADAVRGSWQGVPGHSGAWETSGGHGIFGSQGGLGGQQGNPGGLGTPWVHGYPGNSAGSFGM
NPQGAPWGQGGNGGPPNFGTNTQGAVAQPGYGSVRASNQNEGCTNPPPSGSGGSSNSGGGS
GSQSGSSGSGSNGDNNNGSSSGSSGSSGGSSGGSSGGSSGSGSRRGDSGSESSW
GSSTGSSSGNHGGGGNGHKPGCEKPGNEARGSGESGIQGFRGQGVSSNMREISKEGNRL
GGSGDNYRGQGSSWGSGGDAVGGVNTVNSETSPGMNFDTFWKNFKSKLGFINWDAINKDQ
RSSRIP

```

Signal peptide:

amino acids 1-21

N-glycosylation site.

amino acids 265-269

Glycosaminoglycan attachment site.

amino acids 235-239, 237-241, 244-248, 255-259, 324-328, 388-392

Casein kinase II phosphorylation site.

amino acids 26-30, 109-113, 259-263, 300-304, 304-308

N-myristoylation site.

amino acids 17-23, 32-38, 42-48, 50-56, 60-66, 61-67, 64-70, 74-80, 90-96, 96-102, 130-136, 140-146, 149-155, 152-158, 155-161, 159-165, 163-169, 178-184, 190-196, 194-200, 199-205, 218-224, 236-242, 238-244, 239-245, 240-246, 245-251, 246-252, 249-252, 253-259, 256-262, 266-272, 270-276, 271-277, 275-281, 279-285, 283-289, 284-290, 287-293, 288-294, 291-297, 292-298, 295-301, 298-304, 305-311, 311-317, 315-321, 319-325, 322-328, 323-329, 325-331, 343-349, 354-360, 356-362, 374-380, 381-387, 383-389, 387-393, 389-395, 395-401

Cell attachment sequence.

amino acids 301-304

FIGURE 31

FIGURE 32

MCFLNKLLLLAVLGWLQIPTVPEDLFFLEEGPSYAFEVDTVAPEHGLDNA
CPYIGELRKLLASWVGSSGRSGGFMRKITPTTTSLGAQPSQTSQLQAQLAQAFFHNQPP
SLRRTVEFVAERIGSNCVKHIKATLVADLVRQAESLLQEQLVTQGEEGGDPAQLLEILCSQL
CPHGAQALALGREFCQRKSPGAVRALLPEETPAAVLSSAENIAVGLATEKACAWLSANITAL
IRREVKAASRTLRAQGPEPAARGERRGCSRA

Signal peptide:

amino acids 1-18

N-glycosylation site.

amino acids 244-248

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 89-93

Casein kinase II phosphorylation site.

amino acids 21-25, 167-171, 223-227

N-myristoylation site.

amino acids 100-106, 172-178, 207-213

Microbodies C-terminal targeting signal.

amino acids 278-282

FIGURE 33

TCCCTTGACAGGTCTGGTGGCTGGTCGGGCTACTGAAGGCTGTCTGATCAGGAAACTG
 AAGACTCTCTGCTTTGCCACAGCAGTCTGCAGCTCCTGAGGTGTGAACCCACATCCC
 TGCCCCCAGGGCCACCTGCAGGACGCCGACACCTACCCCTCAGCAGACGCCGGAGAGAA**ATG**
 AGTAGCAACAAAGAGCAGCGGTAGCAGTGTGATCCTCTTGCCTCATCACCATCCT
 CATCCTCTACAGCTCCAACAGTCCAATGAGGTCTTCCATTACGGCTCCCTGCGGGGCCGTA
 GCCGCCGACCTGTCACCTCAAGAAGTGGAGCATCACTGACGGCTATGTCCCCATTCTGGC
 AACAAAGACACTGCCCTCGGTGCCACCAGTGTGATTGTCAGCAGCTCCAGCCACCTGCT
 GGGCACCAAGCTGGGCCCTGAGATCGAGCAGGGCTGAGTGTACAATCCGATGAATGATGCAC
 CCACCACTGGCTACTCAGCTGATGTGGCAACAAGACCACCTACCGCGTCGTGGCCCATTCC
 AGTGTGTTCCCGTGTGAGGAGGCCAGGAGTTGTCACCGGACCCCTGAAACCGTGT
 CATCTCTGGGGGCCCGAGCAAGATGCAGAACGCCAGGGCAGCCTCGTGTGATCC
 AGCGAGCGGGCCTGGTGTCCCCAACATGGAAGCATATGCCGTCTCTCCGGCGATGCG
 CAATTGACGACCTCTCCGGGGTGAGACGGCAAGGACAGGGAGAAGTCTATTGTGGTT
 GAGCACAGGCTGGTTACCATGGTGTGATCGCGGTGGAGTTGTCAGCAGTGTCTATG
 GCATGGTCCCCCCTACTGCAGCCAGCAGGCCGCTCCAGCGCATGCCCTACCAACTAC
 TACGAGCCAAGGGCCGGACGAATGTGTCACCTACATCCAGAATGAGCACAGTCGCAAGGG
 CAACCACCACCGCTCATCCGGGGTGAGACGGCAAGGACAGGGAGAAGTCTATTGTGGCA
 TCACCTTCTCCACCCCTGGACC**TAG**GCCACCCAGCCTGTGGACCTCAGGAGGGTCAG
 AGGAGAAGCAGCCTCCGCCAGCCGCTAGGCCAGGGACCATCTCTGGCCAATCAAGGCTTG
 CTGGAGTGTCTCCAGCCAATCAGGGCTTGAGGAGGATGTATCCTCCAGCCAATCAGGGCC
 TGGGGAACTGTTGGCGAATCAGGGATTGGGAGTCTATGTGGTTAATCAGGGGTGTCTTC
 TTGTGCAGTCAGGGTCTGCGCACAGTCAATCAGGGTAGAGGGGTATTTCTGAGTCAATCTG
 AGGCTAAGGACATGTCCTTCCATGAGGCCTGGTTAGAGCCCCAGGAATGGACCCCCCA
 ATCACTCCCCACTCTGCTGGATAATGGGGCTGTCCAAGGAGCTGGAACTTGGTGTG
 CCCCCCTCAATTCCAGCACCAGAAAAGAGAGATTGTCAGGGGTAGAAGCTGTCTGGAGGCC
 GGCCAGAGAATTGTGGGGTTGTGGAGGTTGTGGGGCGGTGGGGAGGTCCAGAGGTGGGA
 GGCTGGCATCCAGGTCTGGCTCTGCCCTGAGACCTTGACAAACCTCCCCCTCTGGG
 CACCCCTCTGCCACACCAGTTCCAGTGCAGGAGTCTGAGACCCCTTCCACCTCCCTACAA
 GTGCCCTCGGGCTGTCTCCCCGTCTGGACCCCTCCAGCCACTATCCCTGCTGGAAAGGCT
 CAGCTCTTGGGGGTCTGGGGTGACCTCCCCACCTCTGGAAAACCTTGTAGGTATTTG
 GCAAACCTCCTCAGGGTGGGGACTCTGAAGGAAACGGGACAAACCTTAAGCTGTTTCT
 TAGCCCCCTCAGCCAGCTGCCATTAGCTTGGCTCTTAAAGGGCCAGGCCCTCTTCTGCCCT
 CTAGCAGGGAGGTTTCAACTGTTGGAGGCGCCTTGGGCTGCCCTTGTCTGGAGTCA
 CTGGGGCTTCGAGGGTCTCCCTGACCCCTGTCGTCTGGATGGCTGTGGGAGCTGT
 ATCACCTGGGTCTGCTCCCTGGCTGTGATCAGGCACTTATTAAAGCTGGCCTCAGTGG
 GGTGTGTTGTCTGCTCTGGAGGCTGGAAGGAAGGGCTCAGGAGGAGGCTGTGA
 GGCTGGAGGGACCAGATGGAGGAGGCCAGCAGCTAGCCATTGCACACTGGGGTGTGG
 GGGCGGTGACTGCCCACTGGTTGTAAATGATTGTACAGGAATAAACACACACCTACGC
 TCCGGAAAAAAAAAAAAAA

FIGURE 34

MSSNKEQRSAVFVILFALITILILYSSNSANEVFHYGSLRGRSRRPVNLKKWSITDGYVPIL
GNKTLPSRCHQCVIVSSSSHLLGTKLGEIERAECTIRMNDAPTTGYSAVGKTTYRVVAH
SSVFRVLRRPQEFDVNRTPETVFIFWGPPSKMQKPQGSLVRVIQRAGLVFPNMEAYAVSPGRM
RQFDDLFRGETGKDREKSHSWLSTGWFTMVIAVELCDHVHVYGMVPPNYCSQRPRLQRMPYH
YYEPKGPDECVTYIQNEHSRKGNHHRFITEKRVFSSWAQLYGITFSHPSWT

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 9-31 (type II)

N-glycosylation site.

amino acids 64-68, 115-119

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 50-54

Casein kinase II phosphorylation site.

amino acids 3-7, 29-33, 53-57, 197-201

Tyrosine kinase phosphorylation site.

amino acids 253-262

N-myristoylation site.

amino acids 37-43, 114-120, 290-294

FIGURE 35

GTTTCTCATAGTGGCGTCTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
 GAGGGAAAGCATCCCTAGCTGTGGCGAGAGGGCGAGGCTGAAGCCGAGTGGCCAGGGAGGTGTCTGAGGGGCTGG
 GGCAAAAGGTGAAAGAGTTCAAGACAAGCTTCTGGAACCCATGACCCATGAAGTCTTGTGACATTATACCGT
 CTGAGGGTAGCAGCTGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTTTGTGTGACCCCTGGC
 GGCCTATGGGACGTTGGCTTCAGACCTTGTGATAACACC**ATG**CTGCGTGGGACGATGACGGCTGGAGAGGAATG
 AGGCCTGAGGTACACTGGCTTGCCCTCTCTAGCCACAGCAGGCTGCTTGCTGACTTGAACGAGGTCCCTCAG
 GTCACCGTCCAGGCTGCGTCCACCGTCAGAAGCCGGAGGCACTGTGATCTTGGCTGCGTGGTGGAACCTCCA
 AGGATGAATGTAACCTGGCGCTGAATGGGAAAGGAGCTGAATGGCTCGATGATGCTCTGGGTGTCTCATCACC
 CACGGGACCCCTCGTCATCATGCCCCTAACAACCAACACTGTGGGACGGTACCGTGTGGCCGGATGCTGCG
 GGGGCTGTGGCCAGCGTGCAGCCACTGTGACACTAGCCAATCTCAGGACTTCAAGTTAGATGTGCAGCACGTG
 ATTGAAGTGGATGAGGGAAACACAGCAGTCATTGCCACCTGCCAGAGGCCACCCAAAGCCCAGGCCGG
 TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACACCTGATCATGCCCTCAGGGAACCTCCAGATT
 GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGACGCCAACCCAGTGACCCAGGAAGTAAAACC
 TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCGCATCATCTACCCCCCAGAGGCC
 CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGTGCCAGTGGAAATCCACCCCCACGGGTC
 ACCTGGGCAAGGATGGGTCAGGTACCCGGCTACAACAGCAGCGCTCCCTGCTGAGGCAACCTCTCATCGAC
 ACCACCGAGGAGGACTCAGGCACCTACCGCTGATGCCGACAAATGGGGTTGGGAGCCCCGGGAGCGGTC
 ATCCTCTACAATGTCAGGTGTTGAACCCCCCTGAGGTACCATGGAGCTATCCAGCTGGTATCCTGGG
 CAGAGTGCAGGCTTACCTGTGAGGTGCGTGGGAACCCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGCCCC
 CTCATCTCCAGCCAGCGCCTCCGGCTCTCCGCAGGGCCCTGCGCGTGCAGCATGGGCCTGAGGACGAAGGC
 GTCTACCACTGCACTGGCGAGAACAGGAGTGGGAGCGCCATGCCGTAGTCCAGTGCAGCTGCCAGGCAAGC
 ATAACCCCCAAGGCTATGGCAGGATGCTGAGCTGCTACTGCCACACCTCTGTATCACCTCCAAACTCGGCAAC
 CCTGAGCAGATGCTGAGGGGGCAACCGGGCTCCCCAGACCCCCAACGTCAGTGGGCCTGTTCCCCGAAGTGT
 CCAGGAGAGAAGGGGCAAGGGGCTCCCGCCAGGCTCCCATCATCCTCAGCTGCCAGGCAACCTCCAAGACAGAC
 TCATATGAACTGGTGTGGGGCCTCGGCATGAGGGCACTGGCCGGGCCAACCTACTATGTGGTAAACAC
 CGCAAGCAGGTCAAATTCTTGACGATTGGACCATCTCTGGCATTCCAGGCAACCAGCACGCCGTGACCC
 ACCAGACTTGACCCGGGAGCTGTATGAAGTGGAGATGGCAGTTACAACCTGTGCGGGAGAGGGCCAGACAGCC
 ATGGTACCTTCCGAACTGGACGGCGCCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
 GACCCCTGGAGGCCAGTCCCCAGAGCAGCAGCCAGCACGCCGCTCTCCCCCCCCAGAACGCTCCGACAGG
 CCCACCATCTCCACGGCCTCCGGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGGGTTCCCAATC
 CAGTCCCTCCGTGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCACCAGGCCATCCCC
 TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCTACAAGTTGAGTCGGGCTCTGAACATG
 CTGGGGAGAGCGAGGCCAGCGCCCTCTCGGGCCTACGTGGTGTGGCTACAGCGGTGCGTGTACGAGAGG
 CCCGTGGCAGGTCTTATATCACCTTACGGATGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
 CCAGCAAGTAAACAACACCCAAATCCATGGCTTTATATCTTATATCATGACCCACAGACAGTGACAATGATAGT
 GACTACAAGAAGGATATGGTGGAGGGGACAAGTACTGGCACTCCATGCCACCTGGCAGGAGAACCTCCTAC
 GACATTAAGATGCACTGCTTCAATGAAGGAGGGAGAGCAGGTTCAAGCAAGCTGATCTGTGAGGACAAAGCT
 CGGAAGTCTCTGGCCAGCTGGTCACTGCCACCCCAACTCTGGCCCCACCACAGCGGCCCTCTGAAACC
 ATAGAGCGGCCGGTGGCACTGGGCCATGGTGGCTCGCTCCAGCAGCTGCCCTATCTGATTGTCGGGTCGTC
 CTGGGCTCCATGTTCTCATCATCGTCACCTTACCTCCCTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAACAT
 ACAACAGACCTGGGTTTCTCGAAGTGCCCTTCACCCCTCTGCCGTATACTATGGTGCCTGGGAGGACTC
 CCAGGCCACAGGGCAGTGGACGCTACCTCAGTGGCATCAGTGGAGCGGGCTGTGCTAATGGGATCCACATG
 AATAGGGGCTGCCCTCGGTCACTGGGCTACCCGGGCATGAAGCCCCAGCAGCAGCTGCCAGGGGAGCTTCA
 CAGCAGAGTACACCAGCAGCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCCAAAGTCACCA
 ACGAGGGGCTCCAAAGTCTAGCCGGACGAGGGCTTTCTTATACACACTGCCGACGACTCCACTCACCAGCT
 CTGCAAGCCCCATCACGACTGCTGCCAACGCCAGGAGCAGCCCTGCTGCTGTGGCCAGTCAGGGGTGAGGAGGCC
 CCCGAGCTCTGCTGGAGAGCAGTGTGGGACCCCTCATTTCACTCAGGGCCCCCATGCTGCTTGGGCTTGTG
 CCAGTTGAAGAGGGTGGAGCAGTCTCTGCACTGGCAAGTGGAGGGAGACTGGTGTCCCCAGCACCCGTAGGG
 GCCTACGTAGGACAGGAACCTGGAAATGCACTCTCCGGGGGACTGGTGCCTGTGCTTGTGGGAA
 CTCACAAATT**TAG**GCAGAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTTTTTTTTTTTTTT
 AGAGACAGAGAAAATTGGTATTTTCTATTATAGCCATATTATATATTATGCACTTGTAAATAAATGTA
 TATGTTTATAATTCTGGAGAGACATAAGGAGTCTACCGCTGAGGTGGAGAGGGAAAATAAGAAGCTGCCA
 CCTAACAGGAGTCACCCAGGAAGCACCGCACAGGCTGGCGGGACAGACTCCTAACCTGGGCTCTGCAGTG
 GCAGGGGAGGCTGAGGAGGGCCACAGATAAGCTGGCAAGAGGAAGGATCCCAGGCACATGGTCTCATCAGGCA
 TGAGGGAAACAGCAAGGGGCAAGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA
 ACATTTCCTAAGATGCCCATGAGAACAGACCAAGATGTGACAGCACTATGAGCATTAAAAACCTCCAGAAT
 CAATAATCCGTGGCAACATATCTGTAAAAACAAACACTGTAACCTCTAAATAATGTTAGTCTCCCTGTAAAA

FIGURE 36

BIOLOGICAL ASPECTS OF PROTEIN SECRETION

MLRGTTMTAWRGMRPEVTLACLLATAGCFADLNEVPQVTVQPASTVQKPGGTIVILGCVVEPP
 RMNVTVRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTL
 ANLQDFKLDVQHVIEVDEGNTAVIACHLPESHPKAQVRYSVKQEWLEASRGNYLIMPSGNLQ
 IVNASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRSTAEAARIIYPPEAQTIIVTKQSL
 ILECVASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA
 AVILYNQVFEPPEVTMELSQLVIPWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQLRLS
 RRALRVLSMGPEDEGVYQCMAENEVGSAAHVVQLRTSRPSITPRLWQDAELATGTPPVSPSK
 LGNPEQMLRGQPALPRPPTSVGAPSKCPGEKGQQGAPAEAPIIILSSPRTSKTDSYELVWRPR
 HEGSGRAPILYYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGE
 GQTAMVTFRGRRPKPEIMASKEQQIQRDDPGASPQSSSQPDHGRLSPPEAPDRPTISTASE
 TSVYVTWIPRGNGGFPIQSFRVEYKKLKVGDWILATSAIIPPSRLSVEITGLEKGTSYKFRV
 RALNMLGESEPSAPSRYVVSGYSGRVYERPVAGPYITFTDAVNETTIMLKWMYIPASNNT
 PIHGFYIYYRPTSDNDSDYKKDMVEGDKYWHSISHLQPETSYDIKMQCFNEGGESEFSNVM
 ICETKARKSSGQPGRLPPPTLAPPQPLPETIERPVGTGAMVARSDLPYLIVGVVLGSIVL
 IIIVTFIPFCLWRAWSKQKHTTDLGFPRTSALPPSCPYTMOVPLGGLPGHQASGQPYLSGISGRA
 CANGIHMNRGCPAAVGYPGMKPQQHCPGELQQQSDTSSLRQTHLGNGYDPQSHQITRGPK
 SSPDEGSFLYTLPPDDSTHQLLQPHDCCQRQEOPAAGQSGVRRAPDSPVLEAVWDPPFHSG
 PPCCCLGLVPVEEVDSPDSCQVSGGDWCPQHPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 16-30 (type II), 854-879

FIGURE 37

PFOET 3937012014

CGGGAGGCTGGTCGTATGATCCGGACCCCATTGTCGGCCTCTGCCCATGCCTGCTCCTC
 CCAGGCTCCCGCGGCCGACCCCCCGCGAACATGCAGCCCACGGGCCCGAGGGTTCCCGCGC
 GCTCAGCCGGCGGTATCTGCGCGTCTGCTGCTCCTGCTACTGCTGCTGCTGCGGCAGC
 CCGTAACCCGCGCGAGACCACGCCGGCGCCCCAGAGCCCTCTCCACGCTGGCTCCCCC
 AGCCTCTTACCAACGCCGGGTGTCCCCAGCGCCCTCACTACCCCAGGCCTCACTACGCCAGG
 CACCCCCAAAACCTGGACCTTCGGGTCGCGCAGGCCCTGATGCGGAGTTCCCACTCG
 TGGACGGCCACAATGACCTGCCAGGTCTGAGACAGCGTTACAAGAATGTGCTTCAGGAT
 GTTAACCTGCGAAATTTCAGCCATGGTCAGACCAGCCTGGACAGGCTTAGAGACGGCCTCGT
 GGGTGCCCAGTTCTGGTCAGCCTCCGTCTCATGCCAGTCCAGGACCAACTGCCGTGCGCC
 TCGCCCTGGAGCAGATTGACCTCATTCACCGCATGTGTGCCCTACTCTGAACACTGAGCTT
 GTGACCTCAGCTGAAGGTCTGAACAGCTCTCAAAGCTGGCCTGCCTCATTGGCGTNAGGG
 TGGTCACTCACTGGACAGCAGCCTCTGTGCTGCGCAGTTCTATGTGCTGGGTTGCGCT
 ACCTGACACTTACCTCACCTGCAGTACACCATGGCAGAGAGTTCCACCAAGTTCAGACAC
 CACATGTACACCAACGTCAGCGGATTGACAAGCTTGGTGAGAAAGTAGTAGAGGAGTTGAA
 CCGCCTGGCATGATGATAGATTGTCCTATGCATCGGACACCTTGATAAGAAGGGTCTGG
 AAGTGTCTCAGGCTCCTGTGATCTTCTCCACTCAGCTGCCAGAGCTGTGTGACAATTG
 TTGAATGTTCCCGATGATATCCTGCAGCTCTGAAGAACGGTGGCATCGTGTGGACACT
 GTCCATGGGGTGTGCACTGCAACCTGCTGCTAACGTGTCCACTGTGGCAGATCATTG
 ACCACATCAGGGCAGTCATTGGATCTGAGTTCATGGGATTGGTGAAATTATGACGGACT
 GGCCGGTTCCCTCAGGGCTGGAGGATGTGTCACATACCCAGTCCTGATAGAGGAGTTGCT
 GAGTCGTASCTGGAGCGAGGAAGAGCTTCAAGGTGTCCTCGTGGAAACCTGCTGCGGGTCT
 TCAGACAAGTGGAAAAGGTGAGAGAGGGAGAGCAGGGCGCAGAGCCCCGTGGAGGCTGAGTT
 CCATATGGCAACTGAGCACATCCTGCCACTCCCACCTGCGCTCAGAATGGACACCAGGC
 TACTCATCTGGAGGTGACCAAGCAGCCAACCAATGGGCTCCCTGGAGGCTCAAATGCCT
 CCCCATACCTTGTCCAGGCCTGTGGCTGCCACCATCCAACCTCACCCAGTGGCTC
 TGTGACACAGTCGGTCCCCGCAGAGGTCACTGTGGCAAAGCCTCACAAAGCCCCCTCCT
 AGTTCATTACAAGCATATGCTGAGAATAAACATGTTACACATGGAAAA

FIGURE 38

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59817
><subunit 1 of 1, 487 aa, 1 stop, 2 unknown
><MW: 53569.32, pI: 7.68, NX(S/T): 5
MQPTGREGSRALSRRYLRRLLLLLRLQPVTRAETTPGAPRALSTLGSPSLFTTPGVPS
ALTPGLTPGTPKTLDLRGRAQALMRSFPLVDGHNDLPQVLRQRYKNVLQDVNLRNFSGHQ
TSLDLRLDGLVGAQFWSASVSCQSQDQTAVRLALEQIDLIHRMCASYSELELVSAEGLNSS
QKLACLIGVXGGHSDLSSLSVLSFYVLGVRYLTFLTFCSTPWAESSTKFRHHMYTNVSGLT
SFGEKVVEELNRLGMMIDLDSYASDTLIRRVLLEVSQAPVIFSHSAARAVCDNLLNVPDDILQL
LKNGGIVMVTLSMGVLQCNLLANVSTVADHFDHIRAVIGSEFIGIGGNYDGTGRFPQGLEDV
STYPVLIEELLSRXWSEEELQGVLRGNLLRVFRQEVKVREESRAQSPVEAEFPYGQLSTSCH
SHLVPQNGHQATHLEVTKQPTNRVPWRSSNASPYLVPGLVAAATIPTFTQWLC
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

Transmembrane domain:

amino acids 313-331

N-glycosylation sites.

amino acids 119-122, 184-187, 243-246 and 333-336

N-myristylation sites.

amino acids 41-46, 59-64, 73-78, 133-138, 182-187, 194-199, 324-329, 354-359, 357-362, 394-399, 427-432 and 472-477.

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 136-146

FIGURE 39

TGCTAGGCTCTGTCCCACAATGCACCCGAGAGCAGGAGCTGAAAGCCTCTAACACCCACAGA
 TCCCTCTATGACTGCAATGTGAGGTGTCGGCTTGCTGGCCAGCAAGCCTGATAAGC**ATG**
 AAGCTCTTATCTTGGTGGCTGTGGTCGGTGTGCTGGTCCCCAGCTGAAGCCAACAA
 GAGTTCTGAAGATATCCGGTGCAAATGCATCTGTCCACCTTATAGAAAACATCAGTGGCACA
 TTTACAACCAGAATGTATCCCAGAAGGACTGCAACTGCCTGCACGTGGTGGAGCCCATGCCA
 GTGCCTGCCATGACGTGGAGGCCTACTGCCTGCTGCGAGTGCAGGTACGAGGAGCGCAG
 CACCACCACCATCAAGGTCATCATTGTCATCTACCTGTCCGTGGTGGGTGCCCTGTTGCTCT
 ACATGGCCTTCCTGATGCTGGTGGACCCTCTGATCCGAAAGCCGGATGCATACACTGAGCAA
 CTGCACAATGAGGAGGAGAATGAGGATGCTCGCTCTATGGCAGCAGCTGCTGCATCCCTCGG
 GGGACCCCGAGCAAACACAGTCCTGGAGCGTGTGGAAGGTGCCAGCAGCGGTGGAAGCTGC
 AGGTGCAGGAGCAGCGGAAGACAGTCCTCGATCGGCACAAGATGCTCAGC**TAG**ATGGGCTGG
 TGTGGTTGGGTCAAGGCCAACACCATGGCTGCCAGCTCCAGGCTGGACAAAGCAGGGGG
 CTACTTCTCCCTCCCTCGGTTCCAGTCTCCCTTAAAAGCCTGTGGCATTTCCTCCTT
 CTCCCTAACTTTAGAAATGTTGACTTGGCTATTTGATTAGGGAAAGAGGGATGTGGTCTCT
 GATCTCTGTTGCTTCTGGTCTTGGGTTGAAGGGAGGGGAAGGCAGGCCAGAAGGGA
 ATGGAGACATTGAGGCCCTCAGGAGTGGATGCGATCTGTCTCCCTGGCTCCACTCTG
 CCGCCTTCCAGCTCTGAGTCTGGGAATGTTGTTACCTTGGAAAGATAAGCTGGTCTTCA
 GGAACTCAGTGTCTGGAGGAAAGCATGCCAGCATTGAGCATGTGTTCTTCTGCAGTG
 GTTCTTATCACCAACCTCCCTCCAGCCCCGGCGCCTCAGCCCCAGCCCCAGCTCCAGCCCTG
 AGGACAGCTCTGATGGGAGAGCTGGCCCCCTGAGCCCAGTGGCTTCAGGGTGCAGTGG
 AGCTGGTGTTCGCTGCCCCGTGCACTTCTGCACTGGGCATGGAGTGCCATGCATACT
 CTGCTGCCGGTCCCTCACCTGCACTTGAGGGTCTGGCAGTCCCTCTCCCCAGTGT
 CACAGTCACTGAGCCAGACGGTGGTTGGAACATGAGACTCGAGGCTGAGCGTGGATCTGAA
 CACCACAGCCCCGTACTTGGGTTGCCTCTGTCCCTGAACCTCGTTGTAACAGTGCATGGA
 GAGAAAATTTGTCCTTGTCTTAGAGTTGTTGTAATCAAGGAAGCCATCATTAAATTG
 TTTTATTTCTCTCA

4 3 0 0 1 5 2 6 5 7 1 6 4 1 0 1

FIGURE 40

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60278
<subunit 1 of 1, 183 aa, 1 stop
<MW: 20574, pI: 6.60, NX(S/T): 3
MKLLSLVAVVGCLLVPPAEANKSSEDIRCKCICPPYRNISGHYNNQNVSKDCNCLHVVEPM
PVPGHDVEAYCLLCECRYEERSTTTIKVIIIVIYLSVGALLLYMAFLMLVDPLIRKPDAYTE
QLHNEEENEDARSMAAAASLGGPRANTVLERVEGAQQRWKLQVQEQRKTVFDRHKMLS
```

Important features:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 90-112

N-glycosylation sites.

amino acids 21-24, 38-41 and 47-50

FIGURE 41

AGCGGGCTCGTGGGTCGGCTAATTCTGCTGAGGCGTAGACTGAGTTCATAGGGCTGGGTCCCCGA
ACCAGGAAGGGTTAGGGAACACAATCTGCAAGCCCCCGCACCCAAGTGAGGGGCCCTGTTGGGTCTCC
TCCCTTGCACTCCCACCCCTCCGGGCTTGCCTCTCTGGGACCCCTCGCCGGAGATGGCCGCGTGT
CGGAGCAAGGATTCTGCTGCTGCCTACTGGCCGCGGTGCTGATGGTGGAGAGCTCACAGATCGGCAGT
TCGGGCCAAACTCAACTCCATCAAGTCCTCTGGCGGGAGACGCTGGTCAGGCCAATCGATCTGCG
GGCATGTACCAAGGACTGGCATTGGCGCAGTAAGAAGGGAAAACCTGGGCAGGCCTACCTGTAGCAGT
GATAAGGAGTGTGAAGTTGGGAGGTATTGCCACAGTCCCCACCAAGGATCATGGCCTGCATGGTGTGGAGA
AAAAAGAAGCCTGCCACCGAGATGGCATGTGCTGCCAGTACCCGCTGCAATAATGGCATCTGTATCCAGTT
ACTGAAAGCATCTAACCCCTCACATCCGGCTGGATGGTACTCGGCACAGAGATGAAACCACGGTCATTAC
TCAAACCATGACTGGATGGCAGAATCTAGGAAGACCACACTAAGATGTCACATATAAAAGGCATGAAGGA
GACCCCTGCCTACGGATCATCAGACTGCATTGAAGGGTTTGCTGTGCTCGTCATTCTGGACCAAAATGCAAA
CCAGTGCCTCATCAGGGGAAGTCTGTACCAAACAACGCAAGAAGGGTCTCATGGCTGGAAATTTCAGCGT
TGCAGCTGTGCAAGGGCCTGTTGCAAGAGTATGAAAGATGCCACACTCCTCAAAGGCCAGACTCCATGT
TGTCAAGAAAATTTGATTCACCATTGAGGAACATCATCAATTGCAAGACTGTGAAGTTGTGATTAAATGCAATTAG
CATGGTGGAAAATAAGGTTAGATGCAGAAGAATGGCTAAAATAAGAAACGTGATAAGAATATAGATGATCACA
AAAGGGAGAAAGAACATGAACGTGAATAGATTAGAATGGGTGACAAATGCACTGCAGCCAGTGTTCATTATG
CAACTTGTCTATGTAATAATGTACACATTGTTGAAAATGCTATTAAAGAGAACAAAGCACACAGTGGAAATT
ACTGATGAGTAGCATGTACTTCAAGAGTTAGGTTGCTGGAGGAGGGTTCTCAGATTGCTGATTG
TTATACAAAATAACCTACATGCCAGATTCTATTCAACGTTAGGTTAACAAAATACTCCTAGAATAACTGTTA
TACAATAGGTTCTAAAATAAAATTGCTAACAGAACATGGAGCATTGTTAATTACACAGAAAAT
TACCTTTGATTGTAACACTACTCTGCTGTCATCAAGAGCTTGGTAGATAAGAAAAAAATCAGTCATAT
TTCCAAAATAATTGCAAAATAATGCCAGTTGTTAGGAAGGCCATTAGGAAGACAAATAACACAAACAG
CCACAAAATACTTTTCAAAATTAGTTACTGTAATTAAAGAAACTGATACAGACAAAACAGTTCC
TTCAGATTCTACGGAAATGACAGTATATCTCTTTATCTATGTGATTCTGCTGTAATGCATTATATTTC
AACTATACCCATAAAATTGTGACTAGTAAATACTTACACAGAGCAGAATTTCACAGATGGAAAAAATTAAA
GATGTCCAATATATGTGGAAAAGAGCTAACAGAGAGATCATTATTCTAAAGATTGCCATAACCTATATT
GATAGAATTAGATTGGTAAATACATGTATTCAACATACTCTGTTGTAATAGAGACTTAAGCTGGATCTGACTG
CACTGGAGTAAGCAAGAAAATTGGAAAACCTTTCTGTTGTCAGGTTGGCAACACATAGATCATATGTCTG
AGGCACAAGTTGGCTGTTCATCTTGAACACCAGGGAGTCACAGTCTAAATGAATATCTGCATGGATTGCTAT
CATATAATTACTATGCAGATGAATTCACTGAGGCTCTGTCAGGACTATCCTCAAATTATTATTATTTAG
TGCTGAGATCCTCAAATAATCTCAATTCTGAGGTTACAAAAATGACTCCTGAGTAGACAGAGTAGTGAGG
TTCTATTGCCCTCTATAAGCTCTGACTAGCCAATGGCATCATCCAAATTCTCCAAACCTCTGCAGCATCTG
CTTATTGCCAAAGGGCTAGTTCTGGTTCTGCAGCCATTGCCATTAAAAATATAAGTAGGATAACTGTAAA
ACCTGCATATTGCTAAATCTATAGACACCACAGTTCTAAATTCTTGAACCAACTTACTACTTTTAAACTT
AACTCAGTTCTAAATACTTTGCTGGAGCACAAAACAATAAAAGGTTATCTTATAGCTGTGACTTTAAACTTTG
TAGACCACAAATTCACTTTAGTTCTTACTTAAATCCCATCTGCAGTCTCAAATTAAAGTTCTCCAGTAG
AGATTGAGTTGAGGCTGTTATCTTAACTTCAACCTCCCACATATTTACTAAGATGATTAAGACTTA
CATTTCTGCACAGGCTGCAAAACAAAATTATAAAACTAGTCCATCCAAGAACCAAGTTGATTAACACAGGT
TGCTATAAGCTGTGAAATGAAATGGACATTTCAATCAAACATTCTATATAACAAATTATTATTTACAAT
TTGGTTCTGCAATTATTCTTATGTCCACCTTTAAAAAATTATTATTGAAGTAAATTATTACAGGAAATG
TTAATGAGATGTTATTCTTATAGAGATATTCTTACAGAAAGCTTGTAGCAGAATATATTGCACTATTGAC
TTGTAATTAGGAAAATGATAATAAGATAAAATCTATTAAATTTCCTCTAAACTGAAAAAAA
AAAAAAAAAAAAAAAAA

FIGURE 42

MAALMRSKDSSCCLLLAAVLMVESSQIGSSRAKLNSIKSSLGGETPGQAANRSAGMYQGLA
FGGSKKGKNLGQAYPCSSDKECEVGRYCHSPHQGSSACMVCRKKRCHRDGMCCPSTRCNN
GICIPVTEISLTPHIPALDGTRHRDRNIGHYSNHDLGWQNLGRPHTKMSHIKGHEGDPCLRS
SDCIEGFCCARHFWTICKPVLHQGEVCTKQRKKGSHGLEIFQRCDCAKGLSCKVWKDATYS
SKARLHVCQKI

Signal peptide:

amino acids 1-25

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25

FIGURE 43

1000 1500 2000 2500 3000 3500 4000 4500 5000

TCTCAATCTGCTGACCTCGTGTACCGCCTGACCTGTAATCCACCTACCTGGCCTCCAAA
 GTGTTGGGATTACAGGCCGTGAGGCCACCGCGCCGGCAACATCACGTTTAAAAATTGATT
 TCTTCAAATTCATGGCAAATATTCCTCCCTTAACCTCTATGTCAGAATGAGGAAGGA
 TAGCTGCATTTAGTCAGTTCATGCAAGTAATATTCATGTTAGTATTTCTAAG
 TTATATTTAGTAATTCATATGTTAGATTATAGGTTAACATACTTGAAAGAAACTTG
ATGTGTAAAGCCTGGCAGAAATTCTGTATTGTTGAGGATTGTTCTTATCCCCCT
 TTTAAAGTCATCCGTCTGGCTCAGGATTGGAGAGCTTCGACCAACAAAAATGGCAAACA
 TCACCAGCTCCCAGATTTGGACCAGTTGAAAGCTCCGAGTTGGGCCAGTTACCACC
 CCAAGTACACACAGCAGAATAGTACAAGTCACCCCTACAACACTACTACTTCTGGGACCTCAAGCC
 CCCAACATCCCAGTCCTCAGTCCTCAGTCATCTGACTTCAAATCTAACCTGAGCCATCCC
 CAGTTCTAGCCAGTTGAGCCAGCGACAACAGCACCAGAGGCCAGGCAGTCAGTGTCCCTCCT
 CCTGGTTGGAGTCCTTCCTCCAGGCAAAACTCGAGAATCAACACCTGGAGACAGTCC
 CTCCACTGTGAACAAGCTTGCAGCTTCCAGCACGACCATTGAAAATATCTGTGTCTG
 TCCACCAGCCACAGCCAAACACATCAAACATTGCTAACGGCGGATACCCCCAGCTCTAAG
 ATCCCAGCTCTGCAGTGGAAATGCCTGGTCAGCAGATGTCACAGGATTAAATGTGCAGTT
 TGGGGCTCTGGAATTGGGTAGAACCTCTCTCTGAATTGGATCAGCTCCAAGCAGTG
 AAAATAGTAATCAGATCCCAGTCAGCTTGTATTGAAAGTCTTAAGTGAGCCTTGAATACA
 TCTTATCAATGACCAGTGCAGTACAGAACTCCACATATAACACTTCCGTATTACCTCCTG
 CAGTCTGACAAGCTCATCACTGAATTCTGCTAGTCCAGTAGCAATGTCTCCTTATGACC
 AGAGTTCTGTGCATAACAGGATCCCATAACAAAGCCCTGTGAGTCATCAGAGTCAGCTCCA
 GGAACCACATCATGAATGGACATGGGGTGGTCGAAGTCAGCAGACACTAGACAGTAAGTATAG
 CAGCAAGCTACTCTGTATGGCTGGGCCAACAAACAGAGGAAGAGGAGTAGCTCACGTGA
 TGTGGAAAACACCACTGGTCAATGGCTATTGTTAAAGCAGCCCTTTGCTTTTGT
 TTTGGACCAGGTGTTGGCTGTGGTATTAGAAATGTCTTAACCACAGCAAGAAGGAGGT
 GGTGGTCTCATATTCTCTGCCCTAACAGACTGCACCACAAGTCAGCAGCATACAGTATGCAT
 TTTAAAGATGCTTGGCCAGGCAGGGTGGCTGATGCCATAATCCCAGTGCTTGGGGGCC
 AAGGCAGGCAGATTGCCAACAGCTCAGGAGTTGAGACCACCCCTGGCAACATGGTAAACTC
 TGTCTACTAAAATCGAAAAACTAGCCGGGTGTGGTGGCGCGTGCCTGTAATCCCAG
 CTACTTGGGAGGCTGAGGCACAAGAATCGCTTGAGCCAGCTGGCTACAAAGTGAGACTCC
 GTCTGAAAAGA

FIGURE 44

MCFKALGRNSVLLRICSFIPLLKSSVLGSGFELAPPKMANITSSQILDQLKAPSLGQFTTP
PSTQQNSTSHPTTTSWDLKPPTSQSSVLSHLDLKSQPEPSPVLSQLSQRQQHQSQAVTVPP
PGLESFPSQAQLRESTPGDSPSTVNKLLQLPSTTIENISVSVHQQPQPKHIKLAKRRIPASK
IPASAVEMPGSADVTGLNVQFGALEFGSEPSLSEFGSAPSSENSNQIPISLYSKSLSEPLNT
SLSMTSAVQNSTYTTSVITSCSLTSSSLNSASPVAMSSSYDQSSVHNRIPYQSPVSSSESAP
GTIMNGHGGGRSQTLDSKYSSKLLSWLVPTKQRKRIAHMWKTPGQWLIR

Signal peptide:

amino acids 1-24

FIGURE 45

1000 1500 2000 2500 3000 3500 4000 4500 5000

GCCGAGTGGACAAAGCCTGGGCTGGCGGGGGCC**ATG**GCGCTGCCATCCGAATCCTGCT
 TTGGAAACTTGTGCTTCTGCAGAGCTCTGCTGTTCTCCTGCACTCAGCGGTGGAGGAGACGG
 ACGCGGGCTGTACACCTGCAACCTGCACCACACTACTGCCACCTACGAGAGCCTGGCC
 GTCCGCCTGGAGGTACCGACGGCCCCCGGCCACCCCGCCTACTGGGACGGCGAGAAGGA
 GGTGCTGGCGGTGGCGCGCGCACCCCGCCTGACCTGCGTAACCGCAGGGCACGTGT
 GGACCGACCGCACGTGGAGGAGGCTAACAGGTGGTGCACTGGGACCGGCAGCCGCCGGG
 GTCCCGCACGACCGCGGGACCGCCTGCTGGACCTACCGCGTGGCGTGCGGATGCCTTGAGCGCGGTGACT
 TCTCACTGCGTATCGAGCCGCTGGAGGTGGCCACGAGGGCACCTACTCCTGCCACCTGCAC
 CACCAATTACTGTGGCCTGCACGAACGCCGTCTCCACCTGACGGTCGCCAACCCCACGC
 GGAGCCGCCCGGGCTCTCCGGCAACGGCTCCAGCCACAGCGGCCAGGCCCCAGGCCAG
 ACCCCACACTGGCGCGGCCACAACGTATCAATGTCATCGTCCCCGAGAGCCGAGCCCAC
 TTCTTCCAGCAGCTGGCTACGTGCTGGCACGCTGCTGCTTCACTGCTACTGGTCAC
 TGTCTCCTGGCCGCCCGCAGGCCCGAGGCTACGAATACTCGGACCAGAAGTCGGAA
 AGTCAAAGGGGAAGGATGTTAACTTGGGGAGTTGCTGTGGCTGCAGGGACCAGATGCTT
 TACAGGAGTGAGGACATCCAGCTAGATTACAAAAACACATCCTGAAGGAGAGGGCGGAGCT
 GGCCCACAGCCCCCTGCCAGCAACTACATCGACCTAGACAAAGGGTCCGGAAGGAGAACT
GCAAATAGGGAGGCCCTGGCTCCTGGCTGGCTGGCTGGCTGGCAGCTGCACCTCTCTGTGCTC
 CTCGGGCATCTCCTGATGCTCCGGGCTCACCCCTTCCAGCGGCTGGTCCGCTTCC
 GGAATTGGCCTGGCGTATGCAGAGGCCCTCACACCCCTCCCCAGGGCTGGTGG
 AGCATAGCCCCACCCCTGCCCTTGCACGGGTGGCCCTGCCACCCCTGGCACAAACC
 AAAATCCCACGTGATGCCCATCATGCCCTCAGACCCCTCTGGCTCTGCCGCTGGGGCTG
 AAGACATTCTGGAGGACACTCCCACAGAACCTGGCAGCCCCAAACTGGGTGAGCCTCA
 GGGCAGGAGTCCCACTCCTCCAGGGCTCTGCTCGTCCGGGCTGGAGATGTTCTGGAGGA
 GGACACTCCCACAGAACCTGGCAGCCTGAAAGTGGGTGAGCCTCGGCAGGAGTCCCACT
 CCTCCTGGGTGCTGCCACCAAGAGCTCCCCACCTGTACCAACCATGTGGACTCCAG
 GCACCATCTGTTCTCCCCAGGGACCTGCTGACTGAATGCCAGCCCTGCTCCTCTGTGTTG
 CTTGGCCACCTGGGCTGCACCCCTGCCCTTCTGCCACCCCTAGCCTT
 CTCTCAGCCACCTGATAGTCACTGGCTCCCTGTGACTTCTGACCCCTGACACCCCTCC
 GGACTCTGCCTGGCTGGAGTCTAGGGCTGGGCTACATTGGCTCTGTACTGGCTGAGGA
 CAGGGGAGGGAGTGAAGTGGTTGGGCTGTGTTGCCACTCTCAGCACCCACATT
 GCATCTGCTGGTGGACCTGCCACCATCACAATAAGTCCCACATCTGATTTAAAAAAA
 AAAAA

FIGURE 46

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60618
<subunit 1 of 1, 341 aa, 1 stop
<MW: 38070, pI: 6.88, NX(S/T): 1
MALPSRILLWKLVLLQSSAVLLHSAVEETDAGLYTCNLHHHYCHLYESLAVRLEVTDGPPAT
PAYWDGEKEVLAVARGAPALLTCVNRGHVWTDRHVEEAQQVVHWRDQPPGVPHDRADRLLDL
YASGERRAYGPLFLRDRVAVGADAERGDFSLRIEPLEVADEGTYSCHLHHHYCGLHERRVF
HTLVAEPHAEPPEPRGSPGNSSHSGAPGPDTLARGHNVINVIVPESRAHFFQQLGYVIALT
LLFILLLVTLAARRRRGGYEYSDQKSGKSKGDVNLAEEFAVAAGDQMLYRSEDIQLDYKN
NILKERAELAHSPLPAKYIDLKGFRKENCK
```

Important features:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 237-262

N-glycosylation site.

amino acids 205-208

Cell attachment sequence.

amino acids 151-154

Coproporphyrinogen III oxidase proteins.

amino acids 115-140

FIGURE 47

CGCCGGAGGCAGCGGCGGTGGCGCAGCGCGAC**ATGGCCGTTCTCAGAGGACGACTTT**
 CAGCACAGTCAAACCTCACCGAACACAAGCAGCAGTCTCCGAGCTGACCAGGAGGC
 ACTGCTTGAGAAGCTGCTGGACCGCCCCCTGGCCTGCAGAGGCCGAGGACCGCTTCT
 GTGGCACATACATCATCTTCTTCAGCCTGGCATGGCAGTCACTGCCATGGAACTTCTTT
 ATCACTGCCAAGGGAGTACTGGATGTTCAAACACTCCGCAACTCCAGGCCAGCCACGGGGA
 GGACCCCTGAGGGCTCAGACATCCTGAACACTTTGAGAGCTACCTTGCCTGCCTCCACCG
 TGCCCTCCATGCTGTGCCTGGTGGCCAACCTCCTGCTGTCAACAGGGTGCAGTCCACATC
 CGTGTCCCTGGCCTCACTGACGGTACATCCTGGCATCTCATGGTGATAACTGCACTGGTGA
 GGTGGACACTTCCTCCTGGACCCTGGTTTTTGCCTGCCTGACATTGTCTGCATGGTGA
 TCAGCGGTGCCTCCACTGTCTTCAGCAGCAGCATCTACGGCATGACCGGCTCCTTCTATG
 AGGAACCTCCAAGCACTGATATCAGGAGGAGCCATGGGCGGGACGGTCAGCGCCGTGGCCTC
 ATTGGTGGACTTGGCTGCATCCAGTGTGAGGAACAGGCCCTGGCCTTCTGACGG
 CCACCATCTTCCTCGTGCATGGACTCTACCTGCTGTCAGGCTGGAGTATGCC
 AGGTACTACATGAGGCCCTGTTCTTGCGCCCCATGTGTTCTGGTGAAGAGGAGCTTCCCCA
 GGACTCCCTCAGTGCCCTTCGGTGGCCTCCAGATTCAATTGATTCCACACACCCCCCTCTCC
 GCCCCATCCTGAAGAAGACGGCAGCCTGGCTCTGTGTACCTACGTCTTCTCATCACC
 AGCCTCATCTACCCCGCCGTGCACCAACATCGAGTCCCTAACAAAGGGCTCGGGCTCACT
 GTGGACCAACCAAGTTTCATCCCCCTCACTACCTTCCCTGTACAACATTGCTGACCTAT
 GTGGCCGGCAGCTACCGCCTGGATCCAGGTGCCAGGGCCAACAGCAAGGCGCTCCCAGGG
 TTCGTGCTCCTCCGGACCTGCCTCATCCCCCTCTCGTGTCTGTAACTACCAAGCCCCCGT
 CCACCTGAAGACTGTGGCTTCCAGTCCGATGTGTACCCCGACTCCTCAGCTCCCTGCTGG
 GGCTCAGCAACGGCTACCTCAGCACCCCTGGCCCTCTACGGGCTTAAGATTGTGCCAGG
 GAGCTGGCTGAGGCCACGGGAGTGGTGTGCTTTATGTGTGCTGGGCTTAACACTGGG
 CTCAGCCTGCTCTACCCCTGGTCACCTCATC**TAGAAGGGAGGACACAAGGACATTGGT**
 CTTCAGAGCCTTGAAGATGAGAAGAGAGTGCAGGAGGGCTGGGGCCATGGAGGAAAGGCC
 TAAAGTTTCACTGGGACAGAGAGCAGACACTCGGGCTCATCCCTCCAAGATGCCA
 GTGAGCCACGTCCATGCCCATCCGTGCAAGGCAGATATTCCAGTCATATTACAGAACACT
 CCTGAGACAGTTGAAGAAGAAATAGCACAAATCAGGGGTACTCCCTCACAGCTGATGGTTA
 ACATTCCACCTTCTTAGCCCTCAAAGATGCTGCCAGTGTGCTGCCCTAGAGTTATTACA
 AAGCCAGTGCCAAACCCAGCCATGGCTCTTGCAACCTCCAGCTGCCTCATCCAGCT
 GACAGCAGATGCAAGCAAATGCTCAGCTCTTACCCCTGAAGGGCTCCCTGGAATGGA
 AGTCCCTGGCATGGTCAGTCCTCAGGCCAACAGACTCAAGTGTGCACAGACCCCTGTGTTCT
 CGGGGTGAACAACCTGCCACTAACAGACTGGAAAACCCAGAAAGATGGGCTTCCATGAAT
 GCTTCATTCCAGAGGGACCAGAGGGCTCCCTGTGCAAGGGATCAAGCATGTCCTGGCCTGGG
 TTTCAAAAAAAAGAGGGATCCTCATGACCTGGTGTATGGCCTGGGTCAAGATGAGGGTC
 TTTCAGTGTCTGTTACAACATGTCAAAGCCATTGGTTCAAGGGCGTAATAAAACTTGC
 GTATTCAAAAA

6 500152662 11201400

FIGURE 48

MAVVSEDDFQHSSNSTYGTTS defense protein
GSLLPWNFFITAKEYWMFKLRNSSSPATGEDPEGSDILNYFESYLA
VASTVPSMLCLVANFL
LVNRVAHVIRVLASLTVILAIFMVITALVKVDTSSWTRGFFAVTIVCM
VILSGASTVFSSSI
YGMTGSFPMRNSQALISGGAMGGTVSAVASLVDLAASSDVRNSALAFFL
TATIFLVLCMGLY
LLLSRLEYARYYMRPVLAAHVFSGEELPQDSLSAPSVASRFIDSHTPPL
RPILKKTASLGFC
CVTYVFFITSЛИYPAVCTNIESLNKGSGSLWTTKFFIPLTFLLYNFA
DLCGRQLTAWIQVP
GPNSKALPGFVLLRTCLIPLFVLCNYQPRVHLKTVVFQSDVYPALLS
LLGLSNGYLSTLAL
LYGPKIVPRELAEATGVVMSFYVCLGLTLGSACSTLLVHLI

Transmembrane domain:

amino acids 50-74 (type II), 105-127, 135-153, 163-183, 228-252,
305-330, 448-472

FIGURE 49

GACAGTGGAGGGCAGTGGAGAGGACCGCGCTGTCCCTGCTGTCACCAAGAGCTGGAGACACCA
TCTCCCACCGAGAGTCATGCCCCATTGCCCTGCACCTCCTCGTCCTCGTCCCCATCCTCC
TCAGCCTGGTGGCCTCCCAGGACTGGAAGGCTGAACGCAGCCAAGACCCCTTCGAGAAATGC
ATGCAGGATCCTGACTATGAGCAGCTGCTCAAGGTGGTGACCTGGGGCTCAATCGGACCC
GAAGCCCCAGAGGGTATTGTGGTTGGCGCTGGTGTGGCCGGCTGGTGGCCGCCAAGGTGC
TCAGCGATGCTGGACACAAGGTACCACCATCCTGGAGGCAGATAACAGGATCGGGGCCGCATC
TTCACCTACCAGGGACCAGAACACGGGCTGGATTGGGGAGCTGGGAGCCATGCGCATGCCAG
CTCTCACAGGATCCTCCACAAGCTCTGCCAGGGCTGGGCTCAACCTGACCAAGTTCACCC
AGTACGACAAGAACACGTGGACGGAGGTGCACGAAGTGAAGCTGCGCAACTATGTGGTGGAG
AAGGTGCCCGAGAAGCTGGCTACGCCCTGCGTCCCCAGGAAAAGGCCACTGCCCGAAGA
CATCTACCAGATGGCTCTCAACCAGGCCCTCAAAGACCTCAAGGCACTGGCTGCAGAAAGG
CGATGAAGAAGTTGAAAGGCACACGCTCTGGAATATCTTCTCGGGAGGGAACCTGAGC
CGGCCGGCCGTGCAGCTCTGGGAGACGTGATGTCCGAGGATGGCTCTTCTATCTCAGCTT
CGCCGAGGCCCTCCGGGCCCACAGCTGCCAGCGACAGACTCCAGTACAGCCGCATCGTGG
GTGGCTGGGACCTGCTGCCCGCGCTGCTGAGCTCGCTGTCCGGCTTGTGCTGTTGAAC
GCGCCCGTGGTGGCGATGACCCAGGGACCGCACGATGTGCACGTGCAGATCGAGACCTCTCC
CCCGCGCGGAATCTGAAGGTGCTGAAGGCCGACGTGGTGTGCTGACGGCGAGCGGACCGG
CGGTGAAGCGCATCACCTCTGCCCGCTGCCGCCACATGCAGGAGGCCTGCGGGAGG
CTGCACTACGTGCCGCCACCAAGGTGTTCTAACGCTCCGAGGCCCTCTGGCGCGAGGA
GCACATTGAAGGCAGGCCACTCAAACACCGATGCCGCGCATGATTTCTACCGGCCGC
CGCGCGAGGGCGCGCTGCTGCTGGCCTCGTACACGTGGTCGGACGCCGGCAGCGTTCGCC
GGCTTGAGCCGGGAAGAGGCCTTGTGCTGGCGCTGGCGCTCGACGACGTGGCGGATTGCACGGGCC
TGTCGTGCCAGCTCTGGACGGCACCGCGCTCGTCAAGCGTTGGCGGAGGACAGCACA
GCCAGGGTGGCTTGTGGTACAGCCGCCGGCTCTGGCAAACCGAAAAGGATGACTGGACG
GTCCCTTATGGCCGCATCTACTTGCCTGGCGAGCACCGCTACCCGCACGGCTGGGTGGA
GACGGCGGTCAAGTGGCGCTGCCGCCATCAAGATCAACAGCCGGAAAGGGCCTGCGAT
CGGACACGGCCAGCCCCGAGGGCACGCATCTGACATGGAGGGCAGGGCATGTGCATGGG
GTGGCCAGCAGCCCTCGCATGACCTGGCAAAGGAAGAAGGAGCCACCGCTCGCATTAAAGTATTCGGAAAAA
AAA

FIGURE 50

MAPLALHLLVLVPILLSLVASQDWKAERSQDPFEKCMQDPDYEQLLKVVTWGLNRTLKPQRV
IVVGAGVAGLVAAKVLSDAGHKV TILEADNRIGGRIFTYRDQNTGWIGELGAMRMPSSHRL
HKLCQGLGLNLTKFTQYDKNTWTEVHEVKLRNYVVEKPEKLGYALRPQEKGHSPEDIYQMA
LNQALKDLKALGCRKAMKKFERHTLLEYLLGEGNLSPAVQLLGDMSEDGFFYLSFAEALR
AHSCLSDRLQYSRIVGGWDLLPRALLSSLSGLVLLNAPVVAMTQGP HDVHVQIETSPARNL
KVLKADVLLTASGP AVKRITFS PPLPRHMQEALRRLHYVPATKVFLSFRRPFWREEHIEGG
HSNTDRPSRMIFYPPPREGALLSASYTWSAAAAFAGLSREEALRLALDDVAALHGPVRQL
WDGTGVVKRWAEDQHSQGGFVVQPPALWQTEKDDWTVPYGRIVFAGEHTAYPHGWVETAVKS
ALRAAIKINSRKGPASDTASPEGHASDMEGQGHVHG VASSPSHDLAKEEGSHPPVQGQLSLQ
NTTHTRTSH

Signal peptide:

amino acids 1-21

FIGURE 51

CTGACATGGCCTGACTCGGCACAGCTCAGAGCAGGGCAGAACTGGGGACACTCTGGGCCGGCCTCTGCCTGC**AT**
GACGCTCTGAAGCCACCTGTCTCGGAGGAACCACAGAGCAGGGAAAGAAGGACAGGGACTCGTGTGGCAGGAA
 GAACTCAGAGCCGGAAAGCCCCATTCACTAGAACGACTGAGAGATGCGGCCCCCTCGCAGGGCTGAATTTCCT
 GCTGCTGTTCACAAAGATGCTTTATCTTAACCTTTGTTTCCCACCTCCGACCCGGCGTTGATCTGCAT
 CCTGACATTGGAGCTGCCATCTCTGTGGCTGATCACAGACCTCAACCGCTTACCTCTTGACCTGAA
 CAATCAGTCTGTGGATTGAGGGAGGAGCACGGAAAGGGGTTTCCAGAAGAACAAATGACCTAACAAAGTGCTG
 CTTCTCAGATGCCAACGACTATGTATGAGGTTTCCAAGAGGACTCGCTGTGACAATGGGCCCTGCTGGG
 ATATAGAAAACCAAACAGCCCTACAGATGGCTATCTTACAAACAGGTGCTGATAGAGCAGAGTACCTGGGTT
 CTGTCCTTGCATAAGGTATAAATCATCACAGACCGAGTTGTCGGCATCTTGCTCAGAATAGGCCAGAGTG
 GATCATCTCGAATTGGCTGTTACACGTACTCTATGGTAGCTGTACCTCTGTATGACACCTGGGACCAGAAGC
 CATCGTACATATTGCAACAAGGCTGATCGCATGGTGTGACACACCCAAAAGGCATTGGTGCTGAT
 AGGGATGTAGAGAAAGGCTCACCCCGAGCCTGAAGGTGATCATCCTATGGACCCCTTGATGATGACCTGAA
 GCAAAGAGGGGAGAAGAGTGAATTGAGATCTTACCCATATGATGCTGAGAACCTAGGCAAAGAGCACCTCAG
 AAAACCTGTGCCTCCTAGCCCAGAACGACCTGAGCGTCATCTGCTTACCAAGTGGGACCACAGGTGACCCCAAAGG
 AGCCATGATAACCCATCAAATATTGTTCAAATGCTGCTGCCCTCTCAAATGTGTGGAGCATGCTTATGAGCC
 CACTCCTGATGATGTGCCATATCCTACCTCCCTGGCTCATATGTTGAGAGGATTGTACAGGCTGTTGTGTA
 CAGCTGTGGAGCCAGAGTGGATTCTCAAGGGATATTGGTTGCTGGCTGAGGACATGAAGACTTTGAAGCC
 CACATTGTTCCCGCGGTGCCTCGACTCTTAACAGGATCTACGATAAGGTACAAATGAGGCAAGACACCCCT
 GAAGAAGTCTTGTGAAAGCTGGCTGTTCCAGTAAATTCAAAGAGCTCAAAGGGTATCATCAGGCATGATAG
 TTTCTGGGACAAGCTCATCTTGCAAAGATCCAGGACAGCCTGGCGGAAGGGGTTGTAATTGTCACTGGAGC
 TGCCCCATGTCCACTTCAGTCATGACATTCTCCGGCGAGCAATGGGATGTCAGGTGTTGAGCCTTATGGTCA
 AACAGAATGCACAGGTGGCTGTACATTACATTACCTGGGACTGGACATCAGGTACAGTGGTGGGTGCCCTGGC
 TTGCAATTACGTGAAGCTGGAAGATGTGGCTGACATGAACACTTACAGTGAATAATGAAGGAGAGGTCTGCAT
 CAAGGGTACAAACGTTCAAAGGATACTGAGGACAGCCTGGAGAACACAGGAAGCCCTGGACAGTGATGGCTG
 GCTTACACAGGAGACATTGGTCGCTGGCTCCCGAATGGAACACTGAGGATCATGACCCTGGTAAAGAACATT
 CAAGCTGGCCAAGGAGAATACATTGACCCAGAGAAGATAGAAATATCTACAAACAGGAGTCAACAGTGTAA
 AATTGGTACACGGGGAGAGCTTACGGTCATCCTTAGTAGGAGTGGGGTTCTGACACAGATGTTACTCCCTC
 ATTGCAAGCCAAGCTGGGTGAAGGGCTCTTGAGGAACACTGTGCCAAAACCAAGTTGTAAGGGAGGCCATT
 AGAAGACTTGCAAGAAAATTGGGAAAGAAAGTGGCTTAAACCTTTGAAACAGGTCAAAGCCATTTCATCC
 AGAGCCATTTCATTGAAAATGGGCTCTTGACACCAACATTGAAAGCAAAGCGAGGAGAGCTTCAAATACTT
 TCGGACCCAAATTGACAGCCTGTATGAGCACATCCAGGAT**TAGGATAAGGTACTTAAGTACCTGCCGCCACTG**
 TGCACCTGTTGTGAGAAAATGGATTAAAAACTATTCTTACATTGTTGCCCTCCTTATTTTTTAACC
 TGTTAAACTCTAAAGCCATAGCTTTGTTTATATTGAGACATATAATGTGTAACCTAGTTCCAAATAATCA
 ATCCTGCTTCCATCTCGATGTTGTAATATTAAGGCTCAGGGCTACTTTATCAACATGCCTGTCTTCAA
 GATCCCAGTTATGTTCTGTGCTCTCATGATTCCAACCTTAATACTATTAGTAACCACAAGTTCAAGGGT
 CAAAGGGACCTCTGTGCCTCTTGTGATAAACATAACTTGCAACAGTCTATGCTTATTACA
 TCTTCTACTGTTCAAACTAAGAGATTAAATTCTGAAAACACTGCTTACAATTGATGTTCTAGCCACTCCAC
 AAACCAACTAAATTAAATTGTTAGCCTATCACTCATGTCAATCATATCTATGAGACAAATGTCCTCGATGCTCTT
 CTGCGTAAATTAAATTGTTAGCTACTGAAGGGAAAAGCTTGATCATACCAACATTCTCAAACACTCTTAGTTAGATA
 TCTGACTGGGAGTATTAAAATTGGGTCTATGACATACTGTCCAAAAGGAATGCTGTTCTAAAGCATTATT
 CAGTAGGAACCTGGGAGTAATCTGTTCCCTACAGTTGCTGAGCTGGAGCTGGGGAGAGGTGACA
 GGTGGGCCAGTGAACATTCCAGTAAATGAAGCAAGCACTGAATAAAAACCTCTGAACACTGGGAACAAAGATCT
 ACAGGCAAGCAAGATGCCACACAACAGGTTATTCTGTGAAGGAACCAACTGATCTCCCCACCCCTGGATT
 AGAGTTCTGCTTACCTTACCCACAGATAACACATGTTGTTCTACTTGTAATGTAAAGTCTTAAATAAAC
 TATTACAGATAAAAAAA

FIGURE 52

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA60775
<subunit 1 of 1, 739 aa, 1 stop
<MW: 82263, pI: 7.55, NX(S/T): 3
MDALKPPCLWRNHERGKKDRDSCGRKNSEPGSPHSLEALRDAAPSQGLNFLLLFTKMLFIFN
FLFSPLPTPALICILTFGAAIFLWLITRPQPVLPLLDLNQSVGIEGGARKGVSQKNNDLTS
CCFSDAKTMYEVFQRGLAVSDNGPCLGYRKPNQPYRWLSYKQVSDRAEYLGSCLLHKGYKSS
PDQFVGIFAQNRPEWIISELACYTYSMVAAPPLYDTLGPEAIVHIVNKADIAMVICDTPQKAL
VLIGNVEKGFTPSLKVIILMDPFDDDLKQRGEKSGIEILSLYDAENLGKEHFRKPVPPSPED
LSVICFTSGTTGDPKGAMITHQNIVSNAAAFLKCVEHAYEPTPDDVAISYLPALAHMFERIVQ
AVVYSCGARVGFFQGDIRLLADDMKTLKPTLFPAVPRLLNRIYDKVQNEAKTPLKKFLKLA
VSSKFKELOQKGIIRHDSFWDKLIFAKIQDSLGGRVRVIVTGAAPMSTSVMTFRAAMGCQVY
EAYGQTECTGGCTFTLPGDWTSGHGVGPLACNYVKLEDVADMNYFTVNNEGEVCIKGTNVFK
GYLKDPKETQEALDSDGWLHTGDIGRWPNGTLKIIDRKKNIFKLAQGEYIAPEKIENIYNR
SQPVLIQFVHGESLRSSLGVVVVPDTDVLPSFAAKLGVKGSFEELCQNQVVREAILEDLQKI
GKESGLKTFEQVKAIFLHPEPFSIENGLLPTLKAKRGELSKYFRTQIDSPLYEHIQD
```

Important features:**Type II transmembrane domain:**

amino acids 61-80

Putative AMP-binding domain signature.

amino acids 314-325

N-glycosylation site.

amino acids 102-105, 588-591 and 619-622

FIGURE 53

GGAGGGCGGAGGCCGCGCGAGCCGGCCGAGCAGTGAGGGCCCTAGCGGGGCCGAGCGGGG
 CCCGGGGCCCCTAACGCATTCTGAAGTCATGGGCTGGCAGGACATTGGTACCCGCCAAT
 CCGGT**ATG**GACGACTGGAAGCCCAGCCCCCATCAAGCCCTTGGGCTCGGAAGAACGG
 AGCTGGTACCTTACCTGGAAAGTATAAACTGACAAACCAGCGGGCCCTCGGGAGATTCTGTCA
 GACAGGGGCCGTGTTCTGCTGGTACTGTCAATTGTCAATATCAAGTTGATCCTGGACA
 CTCGGCGGCCATCAGTAAGCCAATGAAGACCCAGAGCCAGAGCAAGACTATGATGAGGCC
 CTAGGCCGCTGGAGCCCCACGGCGCAGAGGCACTGGTCCCCGGGGTCTGGACGTAGA
 GGTGTATTCAAGTCGCAGCAAAGTATATGTGGCACTGGATGGCACCGGTGCTGGAGGATG
 AGGCCGGGAGCAGGGCCGGGCATCCATGTCATTGTCCTCAACCAGGCCACGGGCCACGTG
 ATGGCAAACGTGTGTTGACACGTACTCACCTCATGAGGATGAGGCCATGGTGTATTCT
 CAACATGGTAGCGCCGGCCAGTGCTCATCTGCACTGTCAAGGATGAGGCCCTTCCACC
 TCAAGGACACAGCCAAGGCTCTGCTGAGGAGCCTGGCAGCCAGGCTGGCCCTGCCCTGGC
 TGGAGGGACACATGGGCCCTCGTGGGACGAAAAGGAGGTCTGTCTCGGGGAGAAACATT
 TAAGTCACCTGCCCTCTTCTGGGGGACCCAGTCCTGCTGAAGACAGATGTGCCATTGA
 GCTCAGCAGAAGAGGCAGAGTCCACTGGGAGACACAGAGCTGAACCGTCGCCGCCGGCG
 TTCTGCAGCAAAGTTGAGGGCTATGGAAGTGTATGCAGCTGCAAGGACCCCACACCATCGA
 GTTCAGCCCTGACCCACTCCCAGACAACAAGGTCCTCAATGTGCCTGTGGCTGTCAATT
 GGAACCGACCCAATTACCTGTACAGGATGCTGCCTCTGCTTCAAGCCCAGGGGTGTCT
 CCTCAGATGATAACAGTTTCATTGACGGCTACTATGAGGAACCCATGGATGTGGTGGCACT
 GTTGGTCTGAGGGCATCCAGCATCTCCATCAGCATCAAGAATGCCGCTGTCTCAGC
 ACTACAAGGCCAGCCTCACTGCCACTTCAACCTGTTCCGGAGGCCAAGTTGCTGTGGTT
 CTGGAAGAGGACCTGGACATTGCTGTGGATTTTCAGTTCTGAGCCAATCCACCT
 ACTGGAGGAGGATGACAGCCTGTACTGCATCTGCCTGGAATGACCAGGGGTATGAACACA
 CGGCTGAGGACCCAGCACTGTACCGTGTGGAGACCATGCCTGGGCTGGGCTGGGTGCTC
 AGGAGGTCTTGTACAAGGAGGAGCTTGAGCCAAGTGGCCTACACCGGAAAAGCTCTGGGA
 TTGGGACATGTGGATGCGGATGCCGAACAACGCCGGGCCAGAGTGCATCATCCCTGACG
 TTTCCGATCCTACCACTTGGCATCGTGGCCTCAACATGAATGGCTACTTCAAGGAGGCC
 TACTTCAAGAAGCACAAGTTCAACACGGTCCAGGTGTCCAGTCAGGAATGTGGACAGTCT
 GAAGAAAGAAGCTTATGAAGTGGAAAGTTCACAGGCTGCTCAGTGAGGCTGAGGGTCTGGACC
 ACAGCAAGAACCTTGTGAAGACTCTTCTGCCAGACACAGAGGGCCACACCTACGTGGCC
 TTTATTCGAATGGAGAACGATGACTTCACCACCTGGACCCAGCTGCCAAGTGCCTCCA
 TATCTGGACCTGGATGTGCGTGGCAACCACATGGGGCCTGGAGATTGTTGGAAAGAAGA
 ACCACTTCTGGTGGTGGGGTCCCGCTCCCCACTCAGTGAAGAACGCCACCCCTCAGTC
 ACCCCAAATTCTGGAGCCACCCCCAAAGGAGGAGGGAGGCCAGGAGGCCAGAACAGAC
 A**TGA**GACCTCCAGGACCCCTGCGGGCTGGTACTGTGTACCCCAAGGCTGGCTAGCCCT
 TCCCTCCATCCTGTAGGATTTGTAGATGCTGGTAGGGCTGGGCTACCTGTTTTAAC
 TGAGACTTAATTACTAACCAAGGGAGGGTTCCAGTCAGGAAACTGCTGTGGACAGTCT
 AAAAGTCTATTATTTACTTCCTGTTGGAGAACGGCAGGAGAGTACCTGGGAATCATACG
 ATCCCTAGCAGCTCATCCTGCCCTTGAATACCTCACTTCCAGGCTGGCTCAGAACCTA
 ACCTATTTATTGACTGCTCTGAGGGCCTGAAAACAGGCCAACCTGGAGGGCTGGATTTC
 TTTTGGGCTGGAATGCTGCCCTGAGGGTGGGCTGGCTTACTCAGGAAACTGCTGTGCC
 CAACCCATGGACAGGCCAGCTGGGCCACATGCTGACACAGACTCACTCAGAGACCCTA
 GACACTGGACCAGGCCCTCAGCCTCTTGTCCAGATTCCAAGCTGGATAAGTT
 GGTCAATTGATTAAGGAGAACGCCCTGGGAAAAAAAAAAAAAA

FIGURE 54

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA61185
><subunit 1 of 1, 660 aa, 1 stop
><MW: 75220, pI: 6.76, NX(S/T): 0
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RAISEANEDPEPEQDYDEALGRLEPPRRRGSGPDRVLDVEVYSSRSKVVAVDGTTVLEDEA
REQGRGIHVIVLNQATGHVMAKRVFDTYSPEDEAMVLFLNMVAPGRVLICTVKDEGSFHLK
DTAKALLRSLGSQAGPALGWRDTWAFVGRKGGSVGEKHSKSPALSSWGDPVLLKTDVPLSS
AEEAECHWADTELNRLLLLRCSKVEGYGSVCSCDKPTPIEFSPDPLPDNKVLNPVAVIAGN
RPNLYRMLRSLLSAQGVSPQMITSFIDGYEEMDVVALFGLRGIQHTPISIKNARVSQHY
KASLTATFNLFPKAFFVLEEDLDIAVDFLSFLSQSIHLLEEDDSLYCISAWNDQGYEHTA
EDPALLYRVETMPGLGWVLRRSLYKEELEPKWPTPEKLWDWDMWMRMPEQRRGRECIIPDVS
RSYHFGIVGLNMNGYFHEAYFKHKFNTVPGVQLRNDSLKEAYEVHRLLSEAEVLDHS
KNPCEDSFLPDTEGHTYVAFIRMEKDDFTTWTQLAKCLHIWDLVRGNHRGLWRLFRKKNH
FLVVGVPAASPYSVKKPPSVTPIFLEPPPKEEGAPGAPEQT
```

Important features of the protein:

Transmembrane domain:

amino acids 38-55

Homologous region to Mouse GNT1

amino acids 229-660

FIGURE 55

CGGACCGCGTGGGCTGCTGGTGGGAAGGCCTAAAGAACCTGGAAAGCCCCTCTCTTGGAAACCACAC
 CTGTTAAAGAACCTAACGCCATTAAAGCCACTGGAAATTGTTGTCTAGTGGTGTGGGTGAATA
 AAGGAGGGCAGA**ATG**GATTCATCTCCATTAGCCTGCTGTCCTGGCTATGTTGGTGGGATGTTA
 CGTGGCCGGAATCATTCCCTGGCTGTTAATTCTCAGAGGAACGACTGAAGCTGGTACTGTTGG
 GTGCTGGCCTCTGTGGAACTGCTCTGGCAGTCATCGTGCCTGAAGGAGTACATGCCCTTATGAA
 GATATTCTGAGGGAAAACACCAAGCAAGTGAAACACATAATGTGATGCATCAGACAAAGCAGC
 AGAAAAATCAGTTGTCCATGAACATGAGCACAGCCACGACCACACAGCTGCATGCCTATATTGGT
 TTTCCCTCGTTCTGGCTCGTTTCATGTTGCTGGTGGACCAGATTGGTAACTCCCATGTGCATTCT
 ACTGACGATCCAGAAGCAGCAAGGTCTAGCAATTCAAATCACACCCACGCTGGGTCTGGTGTCCA
 TGCTGCAGCTGATGGTGTGCTTGGGAGCAGCAGCATCTACTTCACAGACCAAGTGTCCAGTTAATTG
 TGTTTGTGGCAATCATGCTACATAAGGCACCAGCTGCTTGGACTGGTTCTTCTGATGCATGCT
 GGCTTAGAGCAGAATCGAACATCAGAAAGCACTGCTGGTCTTGCATTGGCAGCACCAGTTATGTCAT
 GGTGACATACTTAGGACTGAGTAAGAGCAGTAAAGAACGCCCTTCAGAGGTGAACGCCACGGAGTGG
 CCATGCTTTCTGCCGGGACATTCTTATGTTGCACAGTACATGTCCTCCCTGAGGTGGCGGA
 ATAGGGCACAGCCACAAGCCGATGCCACGGGAGGGAGAGGCCTCAGCCGCCTGGAAGTGGCAGCCCT
 GGTTCTGGGTTGCCTCATCCCTCATCCTGTCAGTAGGACACCAGCAT**TAA**ATGTTCAAGGTCAGC
 CTTGGTCCAGGGCGTTGCCATCCAGTGAGAACAGCCGGCACGTGACAGCTACTCACTCCTCAGTC
 TCTTGCTCACCTGCGCATCTCTACATGTATTCCCTAGAGTCCAGAGGGAGGTGAGGTTAAACCTG
 AGTAATGGAAAAGCTTTAGAGTAGAAACACATTACGTTGCAAGTTAGCTATAGACATCCCATGTT
 TATCTTTAAAGGCCCTGACATTGCGTTTAATATTCTCTTAACCTATTCTCAGGGAAAGATG
 GAATTAGTTAAGGAAAAGAGGAGAACCTCATACTACAATGAAATAGTGATTATGAAAATACAGT
 GTTCTGTAATTAAAGCTATGCTCTTCTTAGTTAGAGGCTCTGCTACTTATCCATTGATT
 AACATGGTCCCACCATGTAAGACTGGTGCTTAGCATCTATGCCACATGCGTTGATGGAAGGTATA
 GCACCCACTCACTTAGATGCTAAAGGTGATTCTAGTTAATCTGGGATTAGGGTCAGGAAAATGATAGC
 AAGACACATTGAAAGCTCTTTACTCAAAGAGATATCCATTGAAAAGGGATGTCAGAGGGATT
 TAAACAGCTCCTTGGCACGTGCCTCTGGAATCCAGCCTGCCATTCCATCAAATGGAGCAGGAGG
 TGGGAGGGAGCTCTAAAGAGGTGACTGGTATTGTCAGCTTCTAGTTCAAGTTCTCCTTGCGAAAT
 ACCTGTCCTCACATTCTAGAGAGGAGCCAAGTTCTAGTTCAAGGCTTCTCAAGAA
 CAGTCAGATCACAAAGTGTCTTGAAATTAGGGATAATTAAATTAAAGTGTGATTGATGGTTAT
 TGATATCTTGTAGTAGCTTTTAAAGACTACAAAATGTATGGTGTGCTTTTTGTTGTT
 TTTTTTTAATTATTCTCTTAGCAGATCAGCAATCCCTAGGGACCTAAACTAGGTCA
 GGCGACACTGTGCTCTCACATAACCACCTGTAGCAAGATGGATCATAATGAGAAGTGTGTTGCCTA
 TTGATTAAAGCTTATTGGAATCATGTCCTGCTCTCGTCTTTGCTTTCTTCTA
 TCCCTCTAGCCTCTGCCACAATTGCTGCTTACTGCTGGTGTAAATTGTTGTTG
 CTTATCAGGACAACCACTCTCGAACCTGTAATAATGAAGATAATAATCTTATTCTTATCCCT
 CAAAGAAATTACCTTGTGTCAAATGCCGTTGTTGAGCCCTAAACACCACCTCATGTTAA
 ATTGACACAATCACTAATGGTAATTAAACAATTGAGAGTAGCAAAAGTGTAA
 ATTTTTTTCATATTGCCAAAATTGTAACCCCTGTCTGTCAAATAAGTGATAATATTGTAT
 TATTAATTATTACTTCTATACCATTCAAACACATTACACTAAGGGGAACCAAGACTAGTT
 TCTTCAGGGCAGTGGACGTAGTAGTTGTAACCGTTCTATGACGCATAAGCTAGCATGCCTATG
 ATTTATTCTCATGAATTGTCAGTGGATCAGCAGCTGTGGAAATAAGCTTGTGAGCCCTGCT
 GGCCACAGTGAGGAAAGTAGCACAAATAGGATACAGTTGTTGATGTCATTGGCAACAATTG
 ATTTACTACCAAGAGAAGGTATAGTATGGAAAGTCCAAATGACTTCCTGATTGGATGTTAACAGCT
 GACTGGTGTGAGACTTGAGGTTCATCTAGTCCTCAAAACTATATGGTGCCTAGATTCTCTGGA
 AACTGACTTTGTCAAATAATAGCAGATTGTAGTGTCAAAAAAAA

FIGURE 56

MDDFISISLLSLAMLVGCYVAGIIPLAVNFSEERLKLVTVLGAGLLCGTALAVIVPEGVHAL
YEDILEGKHHQASETHNVIASDKAAEKSVVHEHEHSHDHTQLHAYIGVSLVLGFVFMLLVVDQ
IGNSHVHSTDDPEAARSSNSKITTLGLVVHAAADGVALGAAASTSQTSQLIVFVAIMLHK
APAAFGLVSFLMHAGLERNRIRKHLVFALAAPVMSMVTYLGLSKSSKEALSEVNATGVAML
FSAGTFLYVATVHVLPEVGGIGHSHKPDATGGRGLSRLEVAALVLGCLIPPLILSVGHQH

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 37-56, 106-122, 211-230, 240-260, 288-304

FIGURE 57

4500 4500 4500 4500 4500

GCTCGAGGCCGGCGGCGGGAGAGCGACCCGGCCTCGTAGCGGGGCCGGATCCC
 CGAGTGGCGGCCGGAGCCTCGAAAAGAGATTCTAGCGCTGATTTGAG**ATG**ATGGGCTTGG
 GAAACGGGCCTCGCAGCATGAAGTCGCCGCCCTCGTGTGGCCGCCCTGGTGGCCTGCATC
 ATCGTCTTGGGCTTCAACTACTGGATTGCGAGCTCCGGAGCGTGACCTCCAGACACGGAT
 CATGGAGCTGGAAGGCAGGGTCCGCAGGGCGGCTGCAGAGAGAGGCGCCGTGGAGCTGAAGA
 AGAACGAGTTCCAGGGAGAGCTGGAGAACGAGCAGCGGGAGCAGCTTGACAAAATCCAGTCCAGC
 CACAACCTCCAGCTGGAGAGCGTCAACAAGCTGTACCAGGACGAAAAGGCGGTTTGGTGAA
 TAACATCACACAGGTGAGAGGGCTCATCCGAGTGCTGCAAGACCAGTTAAAGACCCTGCAGA
 GGAATTACGGCAGGCTGCAGCAGGATGTCCTCCAGTTAGAAGAACAGACCAACCTGGAG
 AGGAAGTTCTCCTACGACCTGAGCCAGTGCATCAATCAGATGAAGGAGGTGAAGGAACAGTG
 TGAGGAGCGAATAGAAGAGGTACCAAAAAAGGGGAATGAAGCTGTAGCTTCCAGAGACCTGA
 GTGAAAACAACGACCAGAGACAGCAGCTCCAAGCCCTCAGTGAGCCTCAGCCCAGGCTGCAG
 GCAGCAGGCCTGCCACACACAGAGGTGCCACAAGGGAAAGGAAACGTGCTTGGTAACAGCAA
 GTCCCAGACACCAGCCCCAGTCCGAAGTGGTTGGATTCAAAGAGACAAGTTGAGAAAG
 AGGAAACCAATGAGATCCAGGTGGTGAATGAGGAGCCTCAGAGGGACAGGCTGCCAGGAG
 CCAGGCCGGAGCAGGTGGAAAGACAGACCTGTAGGTGGAAGAGGGCTCGGGGGAGCCGG
 AGAACTGGGCCAGACCCCACAGGGTGCAGGCTGCCCTGTCAGTGAGCCAGGAAAATCCAGAGA
 TGGAGGGCCCTGAGCGAGACCAGCTTGTATCCCCGACGGACAGGAGGAGGAGCAGGAAGCT
 GCCGGGGAAAGGGAGAAACCAGCAGAAACTGAGAGGGAGAAGATGACTACAACATGGATGAAAA
 TGAAGCAGAATCTGAGACAGACAAGCAAGCAGCCCTGGCAGGGAATGACAGAAACATAGATG
 TTTTAATGTTGAAGATCAGAAAAGAGACACCATAAATTACTTGATCAGCGTGAAAAGCGG
 AATCATAACACT**TGA**ATTGAACTGGAATCACATTTCACACAGGGCGAAGAGATGACTA
 TAAAATGTTCATGAGGGACTGAATACTGAAAATGTACTAAATAAAATGTACATCTGA

FIGURE 58

MMGLGNGRRSMKSPPVLAALVACIIVLGNYWIASSRSVDLQTRIMELEGRVRRAAAERGA
VELKKNEFQGELEKQREQLDKIQSSHNFQLESVNKLYQDEKAVLVNNITTGERLIRVLQDQL
KTLQRNYGRLQQDVLQFQKNQTNLERKF SYDLSQCINQMKEVKEQCEERIEEVTKKGNEAVA
SRDLSENNNDQRQQLQALSEPQPRLQAAGLPHTEVPGKGNVLGNSQT PAPSSEVVLDSKR
QVEKEETNEIQVVNEEPQRDRLPQEPMREQVVEDRPVGGRGGAGELGQTPQVQAALSVSQ
ENPEMEGPERDQLVIPDGQEEEQEAAGEGRNQQKLRGEDDYNMDENEAESETDKQAALAGND
RNIDVFNVEDQKRDTINLLDQREKRNHTL

Signal peptide:

amino acids 1-29

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29

FIGURE 59

GGATGAGAAAGCTCAGTGTCTTCCTGGCTGGGTCTGCTTCTCTACGCTGGCATGCCCTTCA
CCAGTGGCTTCCTGCTCACCGTTGGAGCTACCAACCATACTGGCTGGATGGCTCCGATTTCGCGGGTTGGTGGCTGA
TGCCATGGGGAGCCAAGGGAAACCTGGGCCTGCTGGATGGCTCCGATTTCGCGGGTTGGTGGCTGA
TAGATGCTCTGCGATTGACTTCGCCAGCCCCAGCATTACACGTGCCTAGAGAGCCTCCTGCTCCCTACCC
TCCTGGCAAACTAAGCTCCTGAGAGGATCCTGGAGATTAGCCCCACCATGCCGGCTCACCGATCTCAGG
TTGACCCCTCCTACCAACCACATGCAGGCCCTAAGGCCCTACCAACTGGCTACTGCCTACCTTATTGATGCTG
GTAGTAACCTGCCAGCCACGCCATAGTGGAGAACATCTCATTAGCAGCTACCAAGTGCAGGAAGGCGTAG
TCTTCATGGAGATGATACTGGAAAGACCTTCTCTGGTCTTCTCAAAGCTTCTTCCCACCTTC
ATGTCAGAGACCTAGACACAGTGGACAATGGCATCTGGAACACCTCTACCCACCATGGACAGTGGTGAATGGG
ACGTGCTGATTGCTCACTTCTGGGTGAGGACACTGTGGCCACAAGCATGGCCCTCACCACCTGAAATGCCA
AGAAAATTAGCCAGATGGACCAGGTGATCCAGGGACTTGTGGAGCGTCTGGAGAATGACACACTGCTGGTAG
CTGGGGACCATGGGATGACCACAAATGGAGACCATGGAGGGACAGTGAGCTGGAGGTCTCAGTGCTCTT
TGTATAGCCCCACAGCAGTCTCCCAAGCACCCACAGAGGAGCCAGAGGTGATTCTCAAGTTAGCCTGTGC
CCACGCTGGCCCTGCTGGCCTGCCATCCATTGGAAATATCGGGGAAGTGTGGCTGAGCTATTCTCAG
GGGGTGAGGACTCCCCAGCCCCACTCCTCTGCTTCTAGGCCAACGCTCAGCTCTCCATCTCAATGTCAGCAGGTGT
CCCCATTCTCATACCTACTCAGCTGTAACCTCAGGCCCTAACGCTAACGGAGCTTCATCAGCTGCAGAACCTCT
TCTCCAAGGCCCTGCTGACTACCAAGTGGCTCTCAGAGGCCAACGGGGCTGAGGCGACACTGCCGACTGTGA
TTGCTGAGCTGCAGCAGTCCCTGCGGGAGCTCGGCCATGTGCATCGAGTCTGGCTCGTTCTCTCTGGTCC
GCATGGGGGGGGTACTGCTCTTGGCTGCTTCTGTTATCTGCCCTGCTGGCATCTCAGTGGCAATATCCC
CAGGGCTTCCATTCTGCCCTACTCCTGACACCTGTGGCCTGGGCTGGGCAATAGCGTATGCTGGAC
TCCTGGGAACTATTGAGCTGAAGCTAGACTAGTCTAGGCTCTAGGGCTGGCTCAGTGAGCTCATTCTCCCTT
TTCTGTGGAAAGCCTGGCTGGCTGGGGTCCAAGAGGCCCTGGCAACCTGTTCTCCCTGGGCCGTCC
TGTTACTCCTGCTGTTGCTGGCTGTTCTCTGATAGTTGTTGAGCTGAGGCCAGGGCACCCCT
TCCTTTGGCTCATTCTGCTGGCTGGCTGGCAGCTCAGTGGAGGGCCAGCTGCTCCACCTAAC
TCACAATGCCCGCCCTGGCACTTCAGCCACAACAAACCCCCCACGGCACAATGGTCATATGCCCTGAGGCTTG
GAATTGGGTGCTTTATGTAAGGCTAGCTGGCTTTTCTCGTGGCCCTGAAGAGACACTGTTGCCACT
CCTCTCCCTGGCTGAGCTCTGGCATCATGGTGGTGGCTGAGCCAAGAATTATGGTATGGAGCTTGTG
GGCGCTGGTGGCCCTGTTAGCTGCCGTGCGCTTGGCTGCCGCTATGTAATCTCAAGAGCCCCGAGCCAC
CCATGCTTTGTGCGCTGGGACTGCCCTAATGGCATTGGTACTGCTGCCACTGGCATTGGCTGGGG
CAGATGAGGCTCCCCCGCTCCGGCTCTGGCTCTGGGCATCCATGGTCTGCCCTGGGTGAGCAGGGC
TGGCTGCTCAGGGCTCGCGCTGCTCTGGAGGCTGTGACAGTGTGGTAAGGCTGGGAGGCCAA
GGACCAGGACTGTCTCACTCCCTCTCAGGCCCCCCTACTTCTCAAGCTGACTTGGATTATGTT
TCTACCGACACATGCAGGAGGAGTCCGGGGCGGTTAGAGAGGACAAATCTCAGGGTCCCTGACTGTGGCTG
CTTATCAGTTGGGAGTGTACTCAGCTGCTATGGTCACAGCCCTCACCTGTTGCCCTCCACTCTGCTGT
TGCATGGAGCGCATCAGCCTGTTCTGCTCTGCTTCTGAGAGCTTCTCTACATCTGCTTG
CTGGGATACCGTCAACCACCCCTGGCTTCTTACTGTGCCATGGCAGGCAGTCTGCCCTGGGCCCTATGCCA
CACAGACCTCTACTCCACAGGCCACAGCCTGCTTCCAGGCCATCCATTGGCATGCA
CAGAGGGTCACTGGCTCTGACTTGGCTGCCCTGCTTAGTGGAGGCAACACCTTGCCTCCACCTCT
TTGCACTGGAGGTTGCCACTGCTCTGCTCTGGCTTCTCTGTTGAGAGCTAAGGGCTGCCGAAGAGACAGCAGC
CCCCAGGGATGAAGCTGATGCCAGAGTCAGACCCGAGGAGGAAGAGGCCACTGATGGAGATGCCCTGGGG
ATGCGCTCAGCACTCTATGCACTGCTGAGCTGGCTGGCCCTAACGTAACCTTCTTCTGTT
TGGCCTGCTGCCCTGGCAGCCTCATCCTGCCAGGCATCTCATGGCTGAAAGTGTGGCCCTAAC
TTGAGGCTGTTGGCTTCAATTGAGCAGCGTGGGACTTCTCTGGCATGAGCTTGTGATTACTGCCACTGGCT
CTGTGAGCTCTGGTCAAGCAGCTATTCTGGCCAGCAGAGGTAGCCTAGTCTGATGTCAG
ACAGAGAGTGTGGAGAACAGTGTAGCCTGGCTGACATCTAGGACTTCAATTCTATAATT
TCTTACTATCATGCAGCCAGGGCCGCTGACATCTAGGACTTCAATTCTATAATT
TGATCCCTAACTCTGATTTGGATGCACTGAGGGACAAGGGGGCGGCTCCGAAGTGGAA
GGCTGGGTGACTTGCAACCTATAATCCCAGCACTTGGGAGGAGGAGGTGGAGGATTGCTTGGT
AGACCAGCCTGTGAAACATAACAAGACCCGCTCTACTATTAAAAAGTGAATAAAATGATAATAT

FIGURE 60

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62809
<subunit 1 of 1, 1089 aa, 1 stop
<MW: 118699, pI: 8.49, NX(S/T): 2
MQKASVLLFLAWVCFLFYAGIALFTSGFLLTRLELTNHSSCQEPPPGPGSLPWGSQGKPGACW
MASRFSRVVLVLIDALRFDFAQHQSHVPREPPVSLPFLGKLSSLQRILEIQPHHARLYRSQ
VDPPTTMQRLKALTGSLPTFIDAGSNFASHAIVEDNLIKQLTSAGRVVFMGDDTWKDLF
PGAFSKAFFPSFNVRDLDTVDNGILEHLYPTMDSGEWDVLIAHFLGVDHCGKHGPHEM
AKKLSQMDQVIQGLVERLENDTLLVAGDHGTTNGDHGGDSELEVSAALFLYSPTAVFPST
PPEEPEVIPQVSLVPTLALLGLPIPGNIGEVMAELFSGGEDSQPHSSALAQASALHLNAQ
QVSRLFHTYSAATQDLQAKELHQLQNLFSKASADYQWLLQSPKGAEATLPTVIAELQQFLRG
ARAMCIESWARFSLVRMAGGTALLAASCFCILLASQWAISPGFPFCPLLLTPVAWGLVGAIA
YAGLLGTIELKLDLVLLGAVAAYVSSFLPFLWKAAGWGSKRPLATLFPIPGPVLLLLFRLA
VFFSDSFVVAEARATPFLLGSFILLVVQLHWEGQLLPPKLLTMPRLGTSATTNPPRHNGAY
ALRLGIGLLLCTRLAGLFHRCPEETPVCHSSPWLSPLASMVGRAKNLWYGACVAALVALLA
AVRLWLRRYGNLKSPEPPMLFVRWGLPLMALGTAAYWALASGADEAPPRLRVLVSGASMVLP
RAVAGLAASGLALLWKPVTVLKAGAGAPRTRTVLTPFSGPPTSQADLDYVVPQIYRHMQE
EFRGRLERTKSQGPLTVAAAYQLGSVYSAAMVTALTLLAFPLLLLHAERISLVFLFLQSFL
LLHLLAAGIPVTPGPFTVPWQAVSAWALMATQTFYSTGHQPVPAIHWHAAFVGFPEGHGS
CTWLPALLVGANTFASHLLFAVGCPLLLWPFLCESQGLRKRQQPPGNEADARVRPEEEEP
LMEMRLRDAPQHFYAALLQLGLKYLFIQILACALAASIIRRHLMVWKVFAPKFIFEAVG
FIVSSVGLLGIALVMRVDGAVSSWFRQLFLAQQR
```

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domains:amino acids 317-341, 451-470, 481-500, 510-527, 538-555, 831-850,
1016-1034, 1052-1070**Leucine zipper pattern.**

amino acids 843-864

N-glycosylation sites.

amino acids 37-40, 268-271

FIGURE 61

1000 1500 2000 2500 3000 3500 4000 4500 5000

TGCCGCTGCCGCCGCTGCTGCTGTTGCTCCTGGCGGCCCTGGGGACGGGCAGTCCCTGT
 GTCTCTGGTGGTTGCCTAACACTGCAAACATCACCTTCTATCCATCAACATGAAGAATGT
 CCTACAATGGACTCCACCAGAGGGTCTCAAGGAGTAAAGTTACTTACACTGTGCAGTATT
 TCATCACAAATTGGCCCACCAGAGGTGGCACTGACTACAGATGAGAAGTCCATTCTGTTGT
 CCTGACAGCTCCAGAGAAGTGGAGAGAAAATCCAGAAGACCTCCTGTTCCATGCAACAAA
 TATACTCCAATCTGAAGTATAACGTGTCTGTTGAATACTAAATCAAACAGAACGTGGTCC
 CAGTGTGTGACCAACCACACGCTGGTGCTCACCTGGCTGGAGCCAACACTCTTACTGCGT
 ACACGTGGAGTCCTCGTCCCAGGGCCCCCTGCCGTGCTCAGCCTCTGAGAAGCAGTGTG
 CCAGGACTTTGAAAGATCAATCATCAGAGTTCAAGGCTAAAATCATCTCTGGTATGTTTG
 CCCATATCTATTACCGTGTTCCTTTCTGTGATGGCTATTCCATCTACCGATATATCCA
 CGTTGGCAAAGAGAACACCCAGCAAATTGATTGATTATGAAATGAAATTGACAAAAA
 GATTCTTGTGCCTGCTGAAAAAAATCGTGATTAACTTATCACCCTCAATATCTGGATGAT
 TCTAAAATTCTCATCAGGATATGAGTTACTGGGAAAAAGCAGTGATGTATCCAGCCTAA
 TGATCCTCAGCCCAGCGGGAACCTGAGGCCCTCAGGAGGAAGAGGGAGGTGAAACATTAG
 GGTATGCTTCGCATTGATGAAATTGGACTCTGAAGAAAACACGGAAGGTACTTCT
 CTCACCCAGCAAGAGTCCCTCAGCAGAACAAATACCCCCGGATAAAACAGTCATTGAATATGA
 ATATGATGTCAGAACCACTGACATTGCGGGGCTGAAGAGCAGGAGCTCAGTTGCAGG
 AGGAGGTGTCCACACAAGGAACATTATTGGAGTCGCAGGCAGCGTTGGCAGTCTGGGCCG
 CAAACGTTACAGTACTCATACACCCCTCAGCTCCAAGACTTAGACCCCTGGCGCAGGAGCA
 CACAGACTCGGAGGAGGGCCGGAGGAAGAGCCATCGACGACCCCTGGTCAGTGGATCCCC
 AAACTGGCAGGCTGTATTCCCTCGCTGTCCAGCTCGACCAGGATTCAAGAGGGCTGCGAG
 CCTTCTGAGGGGGATGGCTCGGAGAGGGAGGTCTTCTATCTAGACTCTATGAGGAGCCGGC
 TCCAGACAGGCCACCAGGAGAAAATGAAACCTATCTCATGCAATTCAATGGAGGAATGGGGT
 TATATGTGCAGATGAAACTGATGCCAACACTCCTTTGCCTTGTGCAAAC
 AAGTGAGTCACCCCTTGATCCCAGCCATAAAGTACCTGGGATGAAAGAAGTTTTCCAGT
 TTGTCAGTGTCTGTGAGAATTACTTATTCTTCTATTCTCATAGCACGTGTGATTG
 GTTCATGCATGTAGGTCTCTAACATGATGGTGGCCTCTGGAGTCCAGGGCTGGCCGGT
 TGTTCTATGCAGAGAAAGCAGTCAATAATGTTGCCAGACTGGGTGCAGAATTATTACAGG
 TGGGTGT

FIGURE 62

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62815
<subunit 1 of 1, 442 aa, 1 stop
<MW: 49932, pI: 4.55, NX(S/T): 5
MSYNGLHQRFKELKLLTLCSSIQQIGPPEVALTTDEKSISVVLTAPEKWKRNPEDLPVSMQ
QIYSNLKYNVSVLNTPSNRTWSQCVTNHTLVLTWLEPNTLYCVHVESFVPGPPRRAQPSEKQ
CARTLKDQSSEFKAKIIFWYVLPISITVFLFSVMGYSIYRYIHVGKEKHPANLILYGNEDF
KRFFVPAEKIVINFITLNISDDSKISHQDMSLLGKSSDVSSLNDPQPSGNLRPPQEEEVKH
LGYASHLMEIFCDSEENTEGTSLTQQESLSRTIPPDKTVIEYEYDVRTTDICAGPEEQELSL
QEEVSTQGTLLESQAALAVLGPQLQYSYTPQLQDLDPLAQEHTDSEEGPEEPSTTLVDWD
PQTGRLCIPSLSSFDQDSEGCEPSEGDGGLGE EGLLSRLYEEPAPDRPPGENETYLMQFMEEW
GLYVQOMEN
```

Important features:

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 140-163

N-glycosylation sites.

amino acids 71-74, 80-83, 89-92, 204-207, 423-426

FIGURE 63

CGGACGCGTGGCGGACGCGTGGCGGACGCGTGGGTCTCTGCAGGGAGACGCCAGCCTGCG
 TCTGCCATGGGGCTCGGGTTGAGGGGCTGGGACGTCCCTGCTGACTGTGCCACGCCCT
 GATGCTGCCGTGAAGCCCCCGCAGGCTCCTGGGGGCCAGATCATGGGGGCCACGAGG
 TGACCCCCACTCCAGGCCCTACATGGCATCCGTGCGCTTCGGGGCAACATCACTGCGGA
 GGCTTCCTGCTGCGAGCCGCTGGTGGTCTGGCCGCCACTGCTTCAGCCACAGAGACCT
 CCGCACTGGCCTGGTGGTCTGGCGCCACGTCCCTGAGTACTGCGGAGCCCACCCAGCAGG
 TGTTGGCATCGATGCTCTCACACGCACCCGACTACCACCCATGACCCACGCCAACGAC
 ATCTGCCTGCTGCGCTGAACGGCTCTGCTGCTGGCCCTGCAGTGGGCTGCTGAGGCT
 GCCAGGGAGAAGGCCAGGCCACAGCAGGGACACGGTGCCGGTGGCTGGCTGGGCT
 TCGTGTCTGACTTGAGGAGCTGCCGCCTGGACTGATGGAGGCCAAGGTCCGAGTGCTGGAC
 CCGGACGTCTGCAACAGCTCCTGGAAGGCCACCTGACACTTACCATGCTCTGCACCCGAG
 TGGGGACAGCCACAGACGGGCTTCTGCTCGGCCACTCCGGAGGGCCCTGGTGTGCAGGA
 ACCGGGCTCACGGCCTGTTCTTCCTCGGCCCTGGTGCAGGCCACCCAAAGACCCCGAC
 GTGTACACGCAGGTGTCCGCCTTGTGGCCTGGATCTGGACGTGGTCTGGCGAGCAGTCC
 CCAGCCCCGCCCCCTGCCTGGACCACCAGGCCAGGAGAAGCCGCCTGAGCCACAACCT
 TGGGGCATGCAAATGAGATGGCCGCTCCAGGCCTGGAATGTTCCGTGGCTGGGCCACGGG
 AAGCCTGATGTTCAAGGTTGGGTGGACGGCAGCGGTGGGCACACCCATTCCACATGCA
 AAGGGCAGAAGCAAACCCAGTAAAATGTTAACTGACAAAAAAAAAAAAAGAAA

FIGURE 64

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62845
><subunit 1 of 1, 283 aa, 1 stop
><MW: 30350, pI: 9.66, NX(S/T): 2
MGLGLRGWGRPLLTVALMLPVKPPAGSWGAQIIGGHEVTPHSRPyMASVRFGGQHCGGF
LLRARWVVAACFSHRDLRTGLVVLGAHVLSAEPQQVFGIDALTTHPDYHPMTHANDIC
LLRLNNGSAVLGPAVGLLRLPGRRARPPTAGTRCRVAGWGFVSDFEELPPGLMEA
VCNSSWKGHLTLMCTRSGDShRRGFCSADSGGPLVCRNRAHGLVSFSGLWCGDPKTPDVY
TQVSAFVAWIWDVVRSSPQPGLPGTTRPPGEAA
```

Signal peptide:

amino acids 1-30

FIGURE 65

GAGCTACCCAGGCGGCTGGTGTGCAGCAAGCTCCGCCTGACTCCGGACGCCCTGACGCCCTGA
 CGCCTGTCCCCGGCCGGC**ATG**AGCCGCTACCTGCTGCCGCTGTCGGCGCTGGGACCGTAG
 CAGGCCTGCCGTGCTGCTCAAGGACTATGTCACCGGTGGGCTTGCCCCAGCAAGGCCACC
 ATCCCTGGAAAGACGGTCATCGTGACGGCGCAACACAGGCATCGGAAGCAGACCGCCTT
 GGAACCTGCCAGGAGAGGAGGAAACATCATCCTGCCCTGCCAGACATGGAGAAGTGTGAGG
 CGGCAGCAAAGGACATCCGCAGGGAGACCCCTCAATCACCATGTCAACGCCGGCACCTGGAC
 TTGGCTTCCCTCAAGTCTATCCGAGAGTTGCAGCAAAGATCATTGAAGAGGAGGAGCGAGT
 GGACATTCTAACTAACAAACGCGGGTGTGATGCGGTGCCCACTGGACCACCGAGGACGGCT
 TCGAGATGCAGTTGGCGTAACCACCTGGTCACTTCTTGTGACAAACTTGCTGCTGGAC
 AAGCTGAAAGCCTCAGCCCCTCGCGGATCATCAACCTCTCGTCCCTGGCCATGTTGCTGG
 GCACATAGACTTTGACGACTTGAACACTGGCAGACGAGGAAGTATAACACCAAAGCCGCTACT
 GCCAGAGCAAGCTGCCATCGCCTCTCACCAAGGAGCTGAGCCGGCGCTGCAAGGCTCT
 GGTGTGACTGTCAACGCCCTGCACCCGGCGTGGCCAGGACAGAGCTGGCAGACACACGGG
 CATCCATGGCTCCACCTCTCCAGCACCAACTCGGGCCCATCTTCTGGCTGCTGGTCAAGA
 GCCCCGAGCTGGCGCCAGCCCAGCACATACCTGGCGTGGCGGAGGAAGTGGCGGATGTT
 TCCGGAAAGTACTCGATGGACTCAAACAGAAGGCCCCGGCCCCGAGGCTGAGGATGAGGA
 GGTGGCCCGGAGGCTTGGCTGAAAGTGCCGCTGGTGGCTTAGAGGCTCCCTGTGA
 GGGAGCAGCCCTCCCCAGA**TAA**ACCTCTGGAGCAGATTGAAAGCCAGGATGGCGCTCCAG
 ACCGAGGACAGCTGCCCATGCCGCAGCTTCTGGCACTACCTGAGCCGGAGACCCAG
 GACTGGCGGCCATGCCGCAGTAGTTCTAGGGGGCGGTGCTGGCGCAGTGGACTGGC
 CTGCAGGTGAGCACTGCCCGGGCTCTGGCTGGTCTGCTCTGCTGCCAGCAGGGAG
 AGGGGCCATCTGATGCTTCCCTGGAAACTAAACTGGGAATGGCCGAGGAGGAAGGGCTC
 TGTGCACTGCAGGCCACGTCAAGGAGAGCCAGCGGTGCCTGTCGGGAGGGTCCAAGGTG
 TCCGTGAAGAGCATGGCAAGTTGTCTGACACTTGGTGGATTCTTGGTCCCTGTGGACCT
 TGTGCATGCATGGCCTCTGAGCCCTGGTTCTCAGCAGTGAAGATGCTCAGAATAACTG
 CTGTCTCCCATGATGGTGTGGTACAGCGAGCTGTTGTCTGGCTATGGCATGGCTGTGCCGG
 GGTGTTGCTGAGGGCTTCCCTGTGCCAGAGCCCAGCCAGAGAGCAGGTGCAGGTGTCATCCC
 GAGTTCAAGGCTTGCACGGCATGGAGTGGAAACCCACCAGCTGCTACAGGACCTGGGA
 TTGCCTGGACTCCCACCTTCTATCAATTCTCATGGTAGTCAAACACTGCAGACTCTCAAAC
 TTGCTCATTT

FIGURE 66

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64842
><subunit 1 of 1, 331 aa, 1 stop
><MW: 35932, pI: 8.45, NX(S/T): 1
MSRYILLPLSALGTVAGAAVLLKDYVTGGACPSKATIPGKTVIVTGANTGIGKQTALELARRG
GNIILACRDMEKCEAAAKDIRGETLNHHVNARHLDLASLKSIREFAAKIIEEEERVDILINN
AGVMRCPHWTTEDGFEMQFGVNHGHFLLTNLLDKLASAPSRIINLSSLAHVAGHIDFDD
LNWQTRKYNTKAAYCQSKLAIVLFTKELSRRLQGSGVTVNALHPGVARTELGRHTGIHGSTF
SSTTLGPIFWLLVKSPELAAQPSTYLVAAELADVSGKYFDGLKQKAPAPEAEDEEVARRLW
AESARLVGLEAPSvreQPLPR
```

Signal peptide:

amino acids 1-17

FIGURE 67

GAAGTCGCGAGCGCTGGC**ATG**TGGCCTGGGCGCGCTGGCGCGCTGCTGGCGGTGCTG
 GCGCTCGGGACAGGAGACCCAGAAAGGGCTGCAGCTCGGGCGACACGTTCTCGCGCTGAC
 CAGCGTGGCGCGGCCCTGGCGCCCGAGCGCCGGCTGCTGGGCTGCTGAGGCGGTACCTGC
 GCGGGGAGGAGGCGCGCTGCAGGACTGACTAGATTCTACGACAAGGTACTTCTTCAT
 GAGGATTCAACAACCCCTGTGGCTAACCTCTGCTGCATTACTCTCATCAAACGCCTGCA
 GTCTGACTGGAGGAATGTGGTACATAGTCTGGAGGCCAGTGAGAACATCCGAGCTCTGAAGG
 ATGGCTATGAGAAGGTGGAGCAAGACCTCCAGCCTTGAGGACCTTGAGGGAGCAGCAAGG
 GCCCTGATGCCGCTGCAGGACGTACATGCTCAATGTGAAAGGCCTGGCCCGAGGTGTCTT
 TCAGAGAGTCAGTGGCTCTGCCATCACTGACCTGTACAGCCCCAACGGCTCTTCTCA
 CAGGGGATGACTGCTCCAAGTGGCAAGGTGGCTATGACATGGGGGATTATTACCATGCC
 ATTCCATGGCTGGAGGAGGCTGTCAGTCCTCCAGGATCTACGGAGAGTGGAAAGACAGA
 GGATGAGGCAAGTCTAGAAGATGCCTGGATCACTGGCCTTGCTTATTCCGGCAGGAA
 ATGTTCTGTGCCCTAGCCTCTCGGGAGTTCTCTACAGCCCAGATAATAAGAGG
 ATGGCCAGGAATGTCTTGAAATATGAAAGGCTCTGGCAGAGAGCCCCAACCACGTGGTAGC
 TGAGGCTGTCATCCAGAGGCCAATATAACCCACCTGCAGACCAGAGACACCTACGAGGGC
 TATGTCAGACCCCTGGGTTCCAGCCCACCTCTACAGATCCCTAGCCTACTGTTCTAT
 GAGACCAATTCCAACGCCTACCTGCTGCTCCAGCCATCCGAAGGAGGTACCCACCTGG
 GCCCTACATTGCTCTACCATGACTTCGTCACTGACTCAGAGGCTCAGAAAATTAGAGAAC
 TTGCAGAACCATGGCTACAGAGGTCACTGGTGGCATCAGGGGAGAAGCAGTTACAAGTGGAG
 TACCGCATCAGCAAAAGTGCCTGGCTGAAGGACACTGTTGACCCAAAATGGTGACCCCTCAA
 CCACCGCATTGCTGCCCTCACAGGCCTTGATGTCCGGCCTCCCTATGCAGAGTATCTGCAGG
 TGGTGAACTATGGCATCGGAGGACACTATGAGCCTCACTTGACCATGCTACGTACCAAGC
 AGCCCCCTACAGAATGAAGTCAGGAAACCGAGTTGCAACATTATGATCTATCTGAGCTC
 GGTGGAAGCTGGAGGAGCCACAGCCTCATCTATGCCAACCTCAGCGTGCCTGTGGTAGGA
 ATGCAGCACTGTTGGGAACCTGCACAGGAGTGGTAAGGGGACAGTGACACACTTCAT
 GCTGGCTGTCCTGTCCTGGTGGAGATAAGTGGTGGCAACAAGTGGATACATGAGTATGG
 ACAGGAATTCCGCAGACCCCTGCAGCTCCAGCCCTGAAGAC**TGA**ACTGTTGGCAGAGAGAAC
 TGGTGGAGTCCTGTGGCTTCCAGAGAAGCCAGGAGCCAAAAGCTGGGTAGGAGAGGAGAA
 AGCAGAGCAGCCTCTGGAAGAAGGCCTGTCAGCTTGCTGTGCCTCGCAAATCAGAGGC
 AAGGGAGAGGTTGTTACAGGGACACTGAGAATGTACATTGATCTGCCAACGGAA
 GTCAGAGTAGGATGCACAGTACAAAGGAGGGGGAGTGGAGGCCTGAGAGGGAAAGTTCTGG
 AGTCAGATACTCTGTTGGGAACAGGGACATCTCAACAGTCTCAGGTTGATCAGTGGTC
 TTTGGCACTTGAAACCTTGACCACAGGGACCAAGAAGTGGCAATGAGGACACCTGCAGGAG
 GGGCTAGCCTGACTCCCAGAACTTAAAGACTTCTCCCCACTGCCTCTGCTGCAGCCAAG
 CAGGGAGTGTCCCCCTCCAGAAGCATATCCCAGATGAGTGGTACATTATAAGGATTTT
 TTTAAGTTGAAAACAACTTCTTTCTTTGTATGATGGTTTTAACACAGTCATTAAGGAA
 ATGTTATAAAATCAAAA

120015883-124104

FIGURE 68

MGPGARLAALLAVLALGTGDPERAARGDTFSALTSGVARALAPERRLLGLLRRYLRGEEARL
RDLTRFYDKVLSLHEDSTTPVANPLLAFTLIKRIQSDWRNVVHSLEASENIRALKDGYEKVE
QDLPAFEDLEGAARALMRLQDVYMLNVKGLARGVFQRVTGSAITDLYSPKRLFSLTGDDCFQ
VGKVAYDMGDYYHAIPWLEEAVSLFRGSYGEWKTEDEASLEDALDHЛАFAYFRAGNVSCALS
LSREFLLYSPDNKRMARNVLKYERLLAESPNHVVAEAVIQRPNIPHQLQTRDTYEGLCQTLGS
QPTLYQIPSLYCSYETNSNAYLLLQPIRKЕVIHLEPYIALYHDFVSDSEAQKIRELAEPWLQ
RSVVASGEKQLQVEYRISKSАWLKDTVDPKLVTLNHRIAALTGLDVRPPYAEYLQVVNYGIG
GHYEPHFDATSPSSPLYRMKSGNRVATFMIYLSSVEAGGATAFIYANLSVPVVRNAALFWW
NLHRSGEGDSDTLHAGCPVLVGDKWVANKWIHEYGQEFRRPCSSPED

Signal peptide:

amino acids 1-19

FIGURE 69

GAGATAGGGAGTCTGGGTTAACGTTCTGCTCCATCTCAGGAGCCCCCTGCTCCCACCCCTAG
 GAAGGCCACCAGACTCCACGGTGTGGGCCAATCAGGTGGAATCGGCCCTGGCAGGTGGGGCC
 ACGAGCGCTGGCTGAGGGACCGAGCCGGAGAGCCCCGGAGCCCCCGTAACCCGCGCAGGGAG
 CGCCCAGG**ATG**CCGCGCGGGACTCGGAGCAGGTGCGCTACTGCGCGCGCTTCTCCTACCTC
 TGGCTCAAGTTTCACTTATCATCTATTCCACCGTGTCTGGCTGATTGGGCCCTGGCCT
 GTCTGTGGGCATCTATGCAGAGGTTGAGCGGCAGAAATATAAAACCTTGAAAGTGCCTTCC
 TGGCTCCAGCCATCATCCTCATCCTCCTGGCGTCGTATGTTCATGGCTCCTCATTGGT
 GTGCTGGCGTCCCTCCGTGACAACCTGTACCTTCCAAGCATTGTACATCCTTGGAT
 CTGCCTCATCATGGAGCTCATTGGTGGCGTGGTGGCCTTGACCTTCCGAAACCAGACCATTG
 ACTTCCTGAACGACAACATTGAAAGAGGAATTGAGAACTACTATGATGATCTGGACTTC
 AACATCATGGACTTTGTTCAAGAAAAGTTCAAGTGCTGTGGCGGGAGGACTACCGAGATTG
 GAGCAAGAATCAGTACCGACTGCAGTGCCTGGACCCCTGGCCTGTGGGTGCCCTACA
 CCTGCTGCATCAGGAACACGACAGAACAGTTGTAACACCATGTGTGGCTACAAACTATCGAC
 AAGGAGCGTTTCAGTGTGCAGGATGTCATCTACGTGCGGGCTGCACCAACGCCGTGATCAT
 CTGGTTCATGGACAACACTACACCATCATGGCGTGCATCCTCCTGGCATTGCTTCCCCAGT
 TCCTGGGGGTGCTGCTGACGCTGCTGTACATCACCCGGTGGAGGACATCATGGAGCAC
 TCTGTCACTGATGGCTCCTGGGCCGGTGCCAAGCCCAGCGTGGAGGCGGCAGGCACGGG
 ATGCTGCTTGTGCTACCCCAAT**TAG**GGCCCAGCCTGCCATGGCAGCTCCAACAAGGACCGTC
 TGGGATAGCACCTCTCAGTCAACATCGTGGGCTGGACAGGGCTGCGGCCCTCTGCCACA
 CTCAGTACTGACCAAAGCCAGGGCTGTGTGCCTGTGTAGGTCCCACGCCCTCTGCCCTC
 CCCAGGGAGCAGGCCTGGGCCTCCCCTAACAGGGCTTCCCCGAGGCAGCTCTGAATCTGT
 GCCCACCTGGGCCTGGGAACAAGGCCCTCTTCTCCAGGCCTGGCTACAGGGAGGGA
 GAGCCTGAGGCTCTGCTCAGGGCCATTTCATCTGGCAGTGCCTGGCGGTGGTATTCAA
 GGCAGTTTGTAGCACCTGTAATTGGGAGAGGGAGTGTGCCCTCGGGCAGGAGGGAAGG
 GCATCTGGGAAGGGCAGGAGGGAAGAGCTGTCCATGCAGCCACGCCATGGCAGGTTGGC
 CTCTTCTCAGCCTCCCAGGTGCCTTGAGCCCTTGTCAAGGGCGCTGCTCCTTGAGCCTA
 GTTTTTTACGTGATTTGTAACATTCACTTTGTACAGATAACAGGAGTTCTGAC
 TAATCAAAGCTGGTATTCCCCGCATGTCTATTGCCCTCCCCAACCAGTTGTTAA
 TCAAACAATAAAACATGTTTGTGTTAAAAAAA

FIGURE 70

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64863
><subunit 1 of 1, 294 aa, 1 stop
><MW: 33211, pI: 5.35, NX(S/T): 3
MPRGDSEQVRYCARFSYWLKFSLIIYSTVFWLIGALVLSVGIVYAEVERQKYKTLESAFLAP
AIILILLGVVMFMVSFIGVLASLRDNLYLLQAFMYILGICLIMELIGGVVALTFRNQTIDFL
NDNIRRGHENYYDDLDFKNIMDFVQKKFKCCGGEDYRDWSKNQYHDCSAPGPLACGVPYTCC
IRNTTEVVNTMCGYKTIDKERFSVQDVIVVRGCTNAVIIWFMDNYTIMACILLGILLPQFLG
VLLTLLYITRVEDIIMEHSVTGLLGPGAKPSVEAAGTGCCLCYPN
```

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 22-42, 57-85, 93-116, 230-257

FIGURE 71

GAGGAGCGGGCCGAGGACTCCAGCGTGCCAGGTCTGGCATCCTGCACTTGCTGCCCTCTGA
 CACCTGGGAAGATGGCCGGCCCGTGGACCTTCACCCTCTGTGGTTGCTGGCAGCCACC
 TTGATCCAAGCCACCCTCAGTCCCCTGCAGTTCTCATCCTCGGCCAAAAGTCATCAAAGA
 AAAGCTGACACAGGAGCTGAAGGACCACAACGCCACCAGCATCCTGCAGCAGCTGCCGCTGC
 TCAGTGCCATGCGGGAAAAGCCAGCCGGAGGCATCCCTGTGCTGGCAGCCTGGTGAACACC
 GTCCTGAAGCACATCATCTGGCTGAAGGTCACTCACAGCTAACATCCTCCAGCTGCAGGTGAA
 GCCCTCGGCCAATGACCAGGAGCTGCTAGTCAAGATCCCCCTGGACATGGTGGCTGGATTCA
 ACACGCCCTGGTCAAGACCATCGTGGAGTTCCACATGACGACTGAGGCCAAGGCCACCATC
 CGCATTGGACACCAGTGCAGTGGCCCCACCCGCCCTGGTCCAGTGAUTGTGCCACCAGCCA
 TGGGAGCCTGCGCATCCAAGTGTATAAGCTCTCCTCCTGGTGAACGCCCTAGCTAACGC
 AGGTCACTGAACCTCCTAGTGCATCCCTGCCAATCTAGTAAAAACCAAGCTGTGTCCCCTG
 ATCGAGGCTTCTCAATGGCATGTATGCAGACCTCCTGCAGCTGGTGAAGGTGCCATTTC
 CCTCAGCATTGACCGTCTGGAGTTGACCTCTGTATCCTGCCATCAAGGGTACACCATTG
 AGCTTACCTGGGGCCAAGTTGGACTCACAGGAAAGGTGACCAAGTGGTCAATAAC
 TCTGCAGCTTCCCTGACAATGCCAACCCCTGGACAACATCCGTTAGCCTCATCGTAGTCA
 GGACGTGGTAAAGCTGCAGTGGCTGCTGTGCTCTCCAGAAGAATTCAATGGTCTGTTGG
 ACTCTGTGCTTCCCTGAGAGTGCCCCTCGGCTGAAGTCAAGCATGGGCTGATCAATGAAAG
 GCTGCAGATAAGCTGGATCTACCCAGATCGTAAGATCCTAACTCAGGACACTCCGAGTT
 TTTTATAGACCAAGGCCATGCCAAGGTGCCAACTGATCGTGCTGGAAGTGGTCCCTCCA
 GTGAAGCCCTCCGCCCTTGTTCACCCCTGGCATCGAAGCCAGCTCGGAAGCTCAGTTTAC
 ACCAAAGGTGACCAACTTAACTCAACTTGAATAACATCAGCTCTGATCGGATCCAGCTGAT
 GAACTCTGGATTGGCTGGTCCAACCTGATGTTCTGAAAAACATCATCACTGAGATCATCC
 ACTCCATCCTGCTGCCGAACCAGAAATGGCAAATTAAAGATCTGGGTCCAGTGTCAATTGGTG
 AAGGCCTTGGGATTGAGGCAGCTGAGTCCTCACTGACCAAGGATGCCCTTGCTTACTCC
 AGCCTCCTGTGAAACCCAGCTCTCTGTCTCCAGTGAAGACTTGGATGGCAGCCATCAG
 GGAAGGCTGGTCCCAGCTGGAGTATGGGTGTGAGCTCTAGACCATCCCTCTGCAAT
 CAATAAACACTTGCCTGTAAAAAA

FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64881
><subunit 1 of 1, 484 aa, 1 stop
><MW: 52468, pI: 7.14, NX(S/T): 3
MAGPWTFTLLCGLLAATLIQATLSPTAVLILGPKVIKEKLTQELKDHNATSILQQPLLSAM
REKPAGGIPLGLSVNTVLKHIWLKVITANILQLQVKPSANDQELLVKIPLDMVAGFNTPL
VKTIVEFHMTTEAQATIRMDTSASGPTRLVLSDCATSHGSLRIQLLYKLSFLVNALAKQVMN
LLVPSLPNLVKNQLCPVIEASFNGMYADLLQLVKVPISLSIDRLEFDLLYPAIKGDTIQLYL
GAKLLDSQGKVTWFNNSAASLTMPILDNIPFSLIVSQDVKAAVAAVLSPEEFMVLLDSVL
PESAHLRKSSIGLINEKAADKLGSTQIVKILTQDTPEFFIDQGHAKVAQLIVLEVFPSSEAL
RPLFTLGIEASSEAQFYTKGDQLILNLNNISSDRIQLMNSGIGWFQPDVLKNIITEIIHSIL
LPNQNGKLRSGVPVSLVKALGFEEAESLTKDALVTPASLWKPSSPVSQ

Important features of the protein:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 48-51, 264-267, 401-404

Glycosaminoglycan attachment site.

amino acids 412-415

LBP / BPI / CETP family proteins.

amino acids 407-457

FIGURE 73

GAGCGAAC**ATG**GCAGCGCGTTGGCGGTTGGTGTCTCTGTGACCAGGTGGTGGCGCTG
 CTCATCGTTGCGACGTTCCCTCAGCCTCTGCCAAAGAAAGAAGGAGATGGTGTATCTGA
 AAAGGTTAGTCAGCTGATGGAATGGACTAACAAAGACCTGTAATAAGAATGAATGGAGACA
 AGTTCGCGCTTGTGAAAGCCCACCGAGAAATTACTCCGTTATCGTCATGTTCACTGCT
 CTCCAAC TG CATAGACAGTGTGCGTTGCAAGCAAGCTGATGAAGAATTCCAGATCCTGGC
 AAACCTCCTGGCGATACTCCAGTGCATTACCAACAGGATA TTTTGCCATGGTGGATTG
 ATGAAGGCTCTGATGTATTCAGATGCTAACATGAATTCACTGAGTACAGGTGCGGGGTTTCAGC
 TGAGCAGATTGCCCGGTGGATGCCGACAGAACTGATGTCAATATTAGAGT GATTAGACCC
 CAAATTATGCTGGTCCCTTATGTTGGGATTGCTTTGGCTTATTGGTGGACTTGTGTAT
 CCTCGAAGAAGTAATATGGAATTCTCTTAATAAAACTGGATGGGCTTTGCAGCTTGTG
 TTTTGTGCTGCTATGACATCTGGTCAAATGTGGAACCATATAAGAGGACCACCATATGCC
 ATAAGAATCCCCACACGGGACATGTGAATTATATCCATGGAAGCAGTCAGGCCAGTTGTA
 GCTGAAACACACATTGTTCTCTGTTAATGGTGGAGTTACCTTAGGAATGGTGCCTTATG
 TGAAGCTGCTACCTCTGACATGGATATTGGAAGCGAAAGATAATGTGTGGCTGGTATTG
 GACTTGTGTATTATTCTTCAGTTGGATGCTCTATTAGATCTAAATATCATGGCTAC
 CCATACAGCTTCTGATGAGT**TAA**AAAGGTCCCAGAGATATAGACACTGGAGTACTGGAA
 ATTGAAAAACGAAAATCGTGTGTTGAAAAGAAGAATGCAACTTGTATATTGTATTAC
 CTCTTTTTCAAGTGATTAAATAGTTAACCTAACAAAGAAGATGTGTAGTGCCTTA
 ACAAGCAATCCTCTGTCATCTGAGGTATTGAAAATAATTATCCTTAACCTCTCTT
 CCCAGTGAACTTATGGAACATTAAATTAGTACAATTAAAGTATATTAAAAATTGTA
 CTACTACTTGTGTTAGTTAGAACAAAGCTCAAACACTTGTAACTTGGTCATCTGAT
 TTTATATTGCCTTATCCAAAGATGGGAAAGTAAGTCCTGACCAGGTGTTCCACATATGCC
 TGTTACAGATAACTACATTAGAATTCTAGCTTCTCATCTTGTGGATGTGTAT
 ACTTACGCATTTCTTGTGAGTAGAGAAATTATGTGTGTCATGTGGTCTCTGAAAATG
 GAACACCATTCTTCAGAGCACACGTCTAGCCCTCAGCAAGACAGTTGTTCTCCTCCT
 GCATATTCTACTGCGCTCCAGCCTGAGTGA TAGAGT GAGACTCTGTCTCAAAAAAGTA
 TCTCTAAATACAGGATTATAATTCTGCTTGAGTATGGTGTAACTACCTGTATTTAGAAA
 GATTTCAGATTCAATTCCATCTCCTTAGTTAAGGTGACCCATCTGTGATAAAAATA
 TAGCTTAGTGCTAAATCAGTGTAACTTACATGGCCTAAATGTTCTACAAATTAGAGT
 TTGTCACTTATTCCATTGTACCTAAGAGAAAAATAGGCTCAGTTAGAAAAGGACTCCCTGG
 CCAGGGCGAGTGA CTTACGCCTGTAATCTCAGCACTTGGGAGGCCAAGGCAGGCAGATCAC
 GAGGTCA GGAGTT CGAGACC ATCTGGCCAACATGGTAAACCCGCTCTACTAAAATAT
 AAAAATTAGCTGGGTGTGGTGGCAGGAGCCTGTAATCCCAGCTACACAGGAGGCTGAGGCAC
 GAGAATCACTGAACTCAGGAGATGGAGGTTCAGTGAGCCGAGATCACGCCACTGCACTCC
 AGCCTGGCAACAGAGCGAGACTCCATCTCAAAAAAAAAAAA

FIGURE 74

MAARWRFWCVSVTMVALIVCDVPSASAQRKKEMVLSEKVSQMEWTNKRPVIRMGDKFR
RLVKAPPRNYSVIVMFTALQLHRQCVVCKQADEEFQILANSWRYSSAFTNRIFFAMVDFDEG
SDVFQMLNMNSAPTFINFPAGKPKRGDTYELQVRGFSAEQIARWIADRTDVNIRVIRPPNY
AGPLMLGLLLAVIGGLVYLRRSNMEFLFNKTGWAFAAALCFVLAMTSQMWNHIRGPPYAHKN
PHTGHVNYIHGSSQAQFVAETHIVLLFNGGVTLMVLLCEAATSMDDIGKRKIMCVAGIGLV
VLFFSWMLSIFRSKYHGYPYSFLMS

Signal peptide:

amino acids 1-29

Transmembrane domains:

amino acids 183-205, 217-237, 217-287, 301-321

FIGURE 75

AAGCAACCAAACGTCAAGCTTGGGAGTTGTCGCTGCCCTGCCGCTCTGCTAGGGAGA
 GAACGCCAGAGGGAGGGCGCTGCCCGGCCAGGCCTCAGAACCGCTACCGGCG**ATG**CTA
 CTGCTGTGGGTGCGGTGCGAGCCTGGCGCTGGCGGTACTGGCCCCGGAGCAGGGGA
 GCAGAGGCAGGAGAGCAGCAAAGCGCCCAATGTGGTGCTGGTGTGAGCGACTCCTCGATG
 GAAGGTTAACATTTCATCCAGGAAGTCAGGTAGTGAAACTCCTTTATCAACTTATGAAG
 ACACGTGGACTTCCTTCTGAATGCCAACAAACTCTCAATTGTTGCCATCACGCGC
 AGCAATGTGGAGTGGCTCTCACTCACTTAACAGAACATCTGGATAATTAAAGGGTAG
 ATCCAAATTATACAACATGGATGGATGTATGGAGAGGCATGGCTACCGAACACAGAAATT
 GGGAAACTGGACTATACTCAGGACATCACTCCATTAGTAATCGTGTGGAAGCGTGGACAAG
 AGATGTTGCTTCTTACTCAGACAAGAAGGCAGGCCATGGTTAATCTTATCCGTAACAGGA
 CTAAAGTCAGAGTGATGGAAAGGGATTGGCAGAACATACAGAACAAAGCAGTAAACTGGTTAAGA
 AAGGAAGCAATTAAATTACACTGAACCATTGTTATTACTGGATTAATTACACACACCC
 TTACCCCTCACCATCTCTGGAGAAAATTGGATCTCAACATTACACATCTTTATT
 GGCTGAAAAAGTGTCTCATGATGCCATCAAAATCCCAAAGTGGTCACCTTGTGAGAAATG
 CACCCCTGTAGATTATTACTCTCTTATACAAAAAAACTGCACGGAAAGATTACAAAAAAAGA
 AATTAAGAACATTAGAGCATTATTATGCTATGTGTGCTGAGACAGATGCCATGCTGGTG
 AAATTATTGGCCCTTCATCAATTAGATCTTCTCAGAAAACATTGTGATATACCTCCTCA
 GACCATGGAGAGCTGGCCATGGAACATCGACAGTTATAAAATGAGCATGTACGAGGCTAG
 TGCACATGTTCCGCTTTGATGATGGGACCAGGAATTAAAGCCGGCTACAAGTATCAAATG
 TGGTTCTCTGGATATTACCCCTACCATGCTGATATTGCTGGAATTCCCTGCCTCAG
 AACCTGAGTGGACTCTTGTGCGTATCATCAGAACATTAAAGAACATGAAACATAAAGT
 CAAAAACCTGCATCCACCCCTGGATTCTGAGTGAATTCCATGGATGTAATGTGAATGCCTCCA
 CCTACATGCTTCGAACTAACCACCTGGAAATATATAGCCTATTGGATGGTGCATCAATTG
 CCTCAACTCTTGATCTTCCCGATCCAGATGAATTACAAATGTTGCTGAAAATTCC
 AGAAATTACTTATTCTTGGATCAGAACGTTCATCCATTATAAAACTACCCCTAAAGTTCTG
 CTTCTGTCCACCAGTATAATAAAAGAGCAGTTATCAAGTGGAAACAAAGTATAGGACAGAAC
 TATTCAAACGTATAGCAAATCTTAGGTGGCACCAAGACTGGCAGAAGGAACCAAGGAAGTA
 TGAAAATGCAATTGATCAGTGGCTAAAACCCATATGAATCCAAGAGCAGTT**TGA**ACAAAAAA
 GTTTAAAATAGTGTCTAGAGACATATAAATATTACAAGATCATAATTATGTATT
 AAATGAAACAGTTAATAATTACCAAGTTTGGCGGGCACAGTGGCTCACACCTGTAATC
 CCAGGACTTGGGAGGCTGAGGAAAGCAGATCACAAGGTCAAGAGATTGAGACCACCTGGC
 CAACATGGTAAACCTGTCTACTAAAAATACAAAAATTAGCTGGCGCGGTGGTGCACA
 CCTATAGTCTCAGCTACTCAGAGGCTGAGGCAGGAGGATCGCTGAACCCGGGAGGCAGCAG
 TTGCAGTGAGCTGAGATTGCGCCACTGTACTCCAGCCTGGCAACAGAGTGGACTGTGCGC
 AAAAATAAAAATAATAATTACCAATTTCATTATTTGTAAGAACATGTAGTG
 TATTGTAAGATAAAATGCCAATGATTATAAAATCACATATTCAAAATGGTTATTATT
 GGCCTTGTACAATTCTAACAAATTAGGTGGAAAGTATCAAAGGATTGAAGCAAATACTGTA
 ACAGTTATGTTCTTTAAATAATAGAGAACATAAAATTGTAATAATATGTATCATAAAAT
 AGTTGTATGTGAGCATTGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAAA

FIGURE 76

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</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64885
<subunit 1 of 1, 536 aa, 1 stop
<MW: 61450, pI: 9.17, NX(S/T): 7
MLLLWVSVVAALALAVLAPGAGEQRRRAAKAPNVVLVVSDFDGRLTFHPGSQVVKLPFINF
MKTRGTSFLNAYTNSPICCPRAAMWSGLFTHLTESWNNFKGLDPNYTTWMDVMERHGYRTQ
KFGKLDYTSGHHSISNRVEAWTRDVAFLRQEGRPMVNLIERNRTKVRVMERDWQNTDKAVNW
LRKEAINYTEPFVIYLGLNLPHYPSPSSGENFGSSTFHTSLYWLEKVSHDAIKIPKWSPLS
EMHPVDYYSSYTKNCTGRFTKKEIKNIRAFYYAMCAETDAMLGEIILALHQLDLLQKTIVIY
SSDHGELAMEHRQFYKMSMYEASAHVPLLMMGPGIKAGLQVSVNVSLVDIYPTMLDIAGIPL
PQNLSGYSLPLSSETFKNEHKVKNLHPPWILSEFHGCNVNASTYMLRTNHWKYIAYSDGAS
ILPQLFDLSSDPDELTNVAVKFPEITYSLDQKLHSIINYPKVSASVHQYNKEQFIKWQSIG
QNYSNVIANLRWHQDWQKEPRKYENAIIDQWLKTHMNPRAV

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Important features:

Signal peptide:

amino acids 1-15

N-glycosylation sites.

amino acids 108-111, 166-169, 193-196, 262-265, 375-378, 413-416,
498-501

Sulfatases proteins:

amino acids 286-315, 359-369, 78-97

FIGURE 77

GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAG
 AGCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCC**ATG**
 GCCTCTCTTGGCCTCCAACTTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTGGGCACACT
 GGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTCTTATGTCGGTGCCAGCATTGTGACAG
 CAGTTGGCTTCTCCAAGGGCTCTGGATGGAATGTGCCACACACAGCACAGGCATCACCCAG
 TGTGACATCTATAGCACCCCTCTGGGCCTGCCCGCTGACATCCAGGCTGCCAGGCCATGAT
 GGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGCATGAGATGCA
 CAGTCTTCTGCCAGGAATCCCAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTC
 ATCCTTGGAGGCCTCTGGGATTCAATTCTGTTGCCTGGAATCTCATGGGATCCTACGGGA
 CTTCTACTCACCACACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTACTTGG
 GCATTATTTCTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTCTGCTCATCC
 CAGAGAAATCGCTCCAACTAACGATGCCAACCTCTGCCACAAGGAGCTC
 TCCAAGGCCTGGTCAACCTCCAAAGTCAAGAGTGAGTTCAATTCTACAGCCTGACAGGGT
 ATGT**TGA**AGAACCAAGGGGCCAGAGCTGGGGGTGGCTGGTCTGTGAAAAACAGTGGACAG
 CACCCCGAGGGCCACAGGTGAGGGACACTACCAACTGGATCGTGTAGAAGGTGCTGCTGAGG
 ATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGCTAGTGTAAACAGCATG
 CAGGTTGAATTGCCAAGGATGCTGCCATGCCAGCCTTCTGTTCTCACCTGCTGCTC
 CCCTGCCCTAACGCCCCAACCTCAACTTGAAACCCATTCCCTAACGCCAGGACTCAGAGG
 ATCCCTTGCCTCTGGTTACCTGGACTCCATCCCCAACCCACTAACATCACATCCACTG
 ACTGACCCCTGTGATCAAAGACCCCTCTCTGGCTGAGGTTGGCTTAGCTCATTGCTGG
 GGATGGGAAGGAGAAGCAGTGGCTTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCC
 TCCAAAGAAACTGATTGCCCTGGAACCTCCATCCACTCTGTTATGACTCCACAGTGTCC
 AGACTAATTGTGCATGAACTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAG
 GATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTAAAAAAATA

FIGURE 78

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64886
><subunit 1 of 1, 230 aa, 1 stop
><MW: 24549, pI: 8.56, NX(S/T): 1
MASLGLQLVGYILGLLGLLGTIVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTGIT
QCDIYSTLLGLPADIQAQAMMVTSAAISLACIISVVGMRCTVFCQESRAKDRVAVAGGVF
FILGGLLGFIPVAWNLHGILRDFYSPLVPSMKFEIGEALYLGISSLFSLIAGIILCFSCS
SQRNRSNYYDAYQAQPLATRSSPRPGQPPKVSEFNSYSLTGYV
```

Important features of the protein:

Signal peptide:

amino acids 1-24

Transmembrane domains:

amino acids 82-102, 117-140, 163-182

N-glycosylation site.

amino acids 190-193

PMP-22 / EMP / MP20 family proteins.

amino acids 46-59

FIGURE 79

GCAC TGCT GCT GTCCC ATCAG CTGCT CTGA AGCT CC **ATG** GTGCC AGA AT CTT CGCT CCT GC
TTAT GTGT CAGT CTGTC CTC CTC TTT GTGT CAAGGG AAGT CATCGCTCCCGCTGGCTCAG
AACCATGGCTGTGCCAGCCGGACCCAGGTGTGGAGACAAGATCTACAACCCCTGGAGCAG
TGCTGTTACAATGACGCCATCGTGTCCCTGAGCGAGACCCGCAATGTGGTCCCCCTGCAC
CTTCTGGCCCTGCTTGAGCTCTGCTGTCTGATTCCCTTGGCCTCACAAACGATTTGTTG
TGAAGCTGAAGGTTCAGGGTGTGAATTCCCAGTGCCACTCATCTCCATCTCCAGTAAATGT
GAAAGCAGAAGACGTTCCC **TGA** GAAGACATAGAAAGAAAATCAACTTCACTAAGGCATC
TCAGAAACATAGGCTAAGGTAAATATGTGTACCAGTAGAGAAGCCTGAGGAATTACAAAATG
ATGCAGCTCCAAGCCATTGTATGGCCATGTGGGAGACTGATGGGACATGGAGAATGACAGT
AGATTATCAGGAAATAATAAGTGGTTTCCAATGTACACACCTGTAAAA

FIGURE 80

MVPRIFAPAYSVCLLCPREVIA PAGSEPWLQCPAPRCGDKIYNPLEQCCYNDAI VSLSE
TRQCGPPCTFWPCFELCCLDSFGLTNDVVKLKVQGVNSQCHSSPISSKCESRRRFP

Signal peptide:

amino acids 1-25

卷之三

FIGURE 81

CTCCACTGCAACCACCCAGAGCCATGGCTCCCCGAGGCTGCATCGTAGCTGTCTTGCCATT
TTCTGCATCTCCAGGCTCCTCTGCTCACACGGAGCCCCAGTGGCCCCATGACTCCTTACCT
GATGCTGTGCCAGCCACACAAGAGATGTGGGGACAAGTTCTACGACCCCCTGCAGCACTGTT
GCTATGATGATGCCGTGCGCCCTGGCCAGGACCCAGACGTGTGGAAACTGCACCTTCAGA
GTCTGCTTGAGCAGTGCTGCCCTGGACCTTCATGGTGAAGCTGATAAACAGAACTGCGA
CTCAGCCGGACCTCGGATGACAGGCTTGTGCGAGTGTCATAATGGAACATCAGGGAA
CGATGACTCCTGGATTCTCCTCCTGGGTGGGCCTGGAGAAAGAGGCTGGTGTACCTGAGA
TCTGGGATGCTGAGTGGCTGTTGGGGCCAGAGAAACACACACTCAA^{CT}GCCCCACTTCATT
CTGTGACCTGCTGAGGCCACCC^{CT}GCAGCTGCC^{CT}GAGGAGGCCACAGGTCCC^{CT}TCTAG
AATTCTGGACAGCATGAGATGCGTGTGCTGATGGGGGCCAGGGACTCTGAACCC^{CT}CCTGAT
GACCC^{CT}TGGCCAACATCAACCCGGCACCA^{CC}CAAGGCTGGCTGGGAACCC^{CT}TCACCC^{CT}
TCTGTGAGATTTCCATCATCTCAAGTTCTCTTCTATCCAGGAGCAAAGCACAGGATCATAA
TAAATTATGTACTTATAAATGAAAA

FIGURE 82

MAPRGCIVAVFAIFCISRLLC SHGAPVAPMTPYLM CQPHKRCGDKFYDPLQHCCYDDAVVP
LARTQTCGNCTFRVC FEQCCPWT FMVKL INQNCD SARTS DDL RLS VS

Signal peptide:

amino acids 1-24

FIGURE 83

GGGGGCGGGTGCCTGGAGCACGGCGTGGGCCGCCGCAGCGCTACTCGCTGCACTCAG
 TCGCGGGAGGCTTCCCCGCGCCGGCGTCCCAGCCGCTCCCCGGCACCAGAAGTCCCT
 GCGCGTCCGACGGCGAC**ATGGCGT**CCCCACGGCCCTGGAGGCCGGCAGCTGGCGCTGGGA
 TCCCTGCTCTCGCTCTTCCCTGGCTGCGTCCCTAGGTCCGGTGGCAGCCTCAAGGTCGC
 CACGCCGTATTCCCTGTATGTCTGTCCCAGGGCAGAACGTACCCACCTGCAGGCT
 TGGGCCCTGTGGACAAAGGGCACGATGTGACCTCTACAAGACGTGGTACCGCAGCTCGAGG
 GGCGAGGTGCAGACCTGCTCAGAGGCCGGCCATCCGAAACCTCACGTTCCAGGACCTCA
 CCTGCACCATGGAGGCCACCAGGCTGCCAACACCAGCCACGACCTGGCTAGCGCCACGGC
 TGGAGTCGGCCTCCGACCACCATGGCAACTTCTCCATCACCATGCGAACCTGACCGCTG
 GATAGCGGCCTCTACTGCTGCCTGGTGGAGATCAGGCACCACACTGGAGCACAGGGT
 CCATGGTGCATGGAGCTGCAGGTGCAGACAGGCCAAAGATGCACCATCCAACGTGTGGT
 ACCCATCCTCCTCCCAGGATAGTGAAAACATCACGGCTGCAGCCCTGGCTACGGGTGCCTGC
 ATCGTAGGAATCCTCTGCCTCCCCCTATCCTGCTCCTGGCTACAAGCAAAGGCAGGCAGC
 CTCCAACCGCCGTGCCAGGAGCTGGTGGATGGACAGCAACATTCAAGGGATTGAAAACC
 CCGGCTTGAAGCCTCACCAACCTGCCAGGGATAACCGAGGCCAAAGTCAGGCACCCCTG
 TCCTATGTGGCCCAAGCGGCAGCCTCTGAGTCTGGCGGCATCTGCTTCGGAGCCCAGCAC
 CCCCCTGTCTCCTCCAGGCCCGGAGACGTCTTCCATCCCTGGACCCGTCCCTGACT
 CTCCAAACTTGAGGTATC**TAG**CCCAGCTGGGGACAGTGGCTGTTGGCTGGGCTGG
 GGCAGGTGCATTGAGCCAGGGCTGGCTGTGAGTGGCTCCTGGCCTCGGCCCTGGTC
 CCTCCCTCCTGCTCTGGCTCAGATACTGTGACATCCCAGAACGCCAGCCCTAACCCCTC
 TGGATGCTACATGGGATGCTGGACGGCTCAGCCCTGTTCAAGGATTGGGTGCTGAG
 ATTCTCCCTAGAGACCTGAAATTCAACCAGCTACAGATGCCAAATGACTTACATCTTAAGAA
 GTCTCAGAACGTCCAGCCCTCAGCAGCTCTGTTCTGAGACATGAGCCTGGATGTGGCA
 GCATCAGTGGACAAGATGGACACTGGGCCACCCCTCCAGGCACCAGACACAGGGCACGGT
 GAGAGACTCTCCCCGTGGCCCTGGCTCCCCGTTGCCCAGGTGCTCTCTGTC
 AGACTTCCTTTGTACCACAGTGGCTGGGCCAGGCCTGCCCTGCCACTGGCCATGCC
 ACCTTCCCCAGCTGCCTCCTACCAGCAGTTCTGAAGATCTGCAACAGGTTAAGTCAAT
 CTGGGCTTCACTGCCTGCATTCCAGTCCCCAGAGCTGGTGGTCCCAGGGAAAGTAC
 ATATTGGGCATGGTGGCCTCCGTGAGCAAATGGTGTCTGGCAATCTGAGGCCAGGACAG
 ATGTTGCCCAACCCACTGGAGATGGTGCTGAGGGAGGTGGTGGGCCCTGGAAAGGTGA
 GTGGAGAGGGGCACCTGCCCTCCCTCCCATCCCTACTCCACTGCTCAGCGCGGGCC
 ATTGCAAGGGTGCCACACAATGTCTGTCCACCCCTGGGACACTTCTGAGTATGAAGCGGGAT
 GCTATTAAAAACTACATGGGAAAAAAAAAAAAAAAAAAAAAAAAGA

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

FIGURE 84

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64897
><subunit 1 of 1, 311 aa, 1 stop
><MW: 33908, pI: 6.87, NX(S/T): 6
MGVPTALEAGSWRWGSLLFALFLAASLGPVAAFKVATPYSLYVCPEGQNVTLTCRLLGPVDK
GHDVTFYKTWYRSSRGEVQTCSEERRPIRNLTFQDLHLHHGGHQAANTSHDLAQRHGLESASD
HHGNFSITMRNLTLLDSGLYCCLVVEIRHHHSEHRVHGAMELQVQTGKDAPSNCVVYPSSQ
DSENITAAALATGACIVGILCLPLLLLLVYKQRQAASNRRAQELVRMDSNIQGIENPGFEAS
PPAQGIPEAKVRHPLSYVAQRQPSESGRHLLSEPSTPLSPPPGDVFFPSLDPPDSPNFEVI
```

Signal peptide:

amino acids 1-28

Transmembrane domain:

amino acids 190-216

FIGURE 85

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100

CCCACGCGTCCGCGCCTCTCCCTCTGCTGGACCTTCCTCGTCTCCATCTCTCCCTCCT
 TTCCCCCGTTCTCTTCCACCTTCTCTTCTTCCCACCTAGACCTCCCTCCCTGCCCTCC
 TTTCTGCCAACGCTGCTCCCTGGCCCTCTCCGACCCGCTTAGCAGCAGACCTCCTGG
 GGTCTGTGGGTTGATCTGTGGCCCTGTGCCTCCGTGTCCTTGTCTCCCTCCCTCCGA
 CTCCGCTCCGGACCAGCGGCCTGACCTGGGAAAGG**ATG**GTTCCCGAGGTGAGGGTCCTC
 TCCTCCTTGCTGGACTCGCGCTGCTCTGGTCCCCCTGGACTCCCACGCTCGAGCCGCC
 AGACATGTTCTGCCTTTCCATGGAAAGAGATACTCCCCCGCGAGAGCTGGCACCCCTACT
 TGGAGCCACAAGGCCTGATGTACTGCCTGCGCTGTACCTGCTCAGAGGGCGCCCATGTGAGT
 TGTTACCGCCTCCACTGTCCGCCTGTCCACTGCCCTCAGCCTGTGACGGAGCCACAGCAATG
 CTGTCCAAGTGTGGAACCTCACACTCCCTCTGGACTCCGGGCCCCACCAAAGTCCTGCC
 AGCACAAACGGGACCATGTACCAACACGGAGAGATCTCAGTGCCTGAGCTGTTCCCTCC
 CGCCTGCCAACCAACCAGTGTGTCCTCTGCAGCTGCACAGAGGGCCAGATCTACTGC
 AACCTGCCCGAACCAAGGCTGCCAGCACCCCTCCACTGCCAGACTCCTGCTGCCAAC
 GCAAAGATGAGGAAGTGAAGCAATCGGATGAAGAGGACAGTGTGCAGTCGCTCCATGGGTG
 AGACATCCTCAGGATCCATGTTCCAGTGTGCTGGAGAAAGAGAGGGCCGGCACCCAGC
 CCCCACGGCTCAGGCCCTCTGAGCTTCATCCCTGCCACTTCAGACCCAAGGGAGCAG
 GCAGCACAACTGTCAAGATCGCCTGAAGGAGAAACATAAGAAAGCCTGTGTCATGGCGG
 AAGACGTACTCCCACGGGAGGTGTGGCACCCGGCTTCCGTGCCTCGGCCCTTGCCCTG
 CATCCTATGCACCTGTGAGGATGCCGCCAGGACTGCCAGCGTGTGACCTGTC
 ACCCGCGTCACCCCGAGAAAGTGGCTGGGAAGTGCTGCAAGATTGCCAGAGGACAAA
 GCAGACCCCTGGCCACAGTGAGATCAGTTCTACCAGGTGTCCAAGGCACCGGGCGGG
 CGTCCACACATCGGTATCCCCAAGCCCAGACAACCTGCGTCGCTTGCCCTGGAACAC
 CCTCGGACTTGGAGATCTACCTCTGGAAGCTGGTAAAGATGAGGAAACTGAGGCTCAG
 AGAGGTGAAGTACCTGGCCAAGGCCACACAGCCAGAATCTTCCACTTGACTCAGATCA
 AAGTCAGGAAGCAAGACTCCAGAAAGAGGCACAGCACTCCGACTGCTCGCTGG
 GAAGGTCACTGGAACGTCTCCTAGCCCAGACCTGGAGCTGAAGGTACGCCAGTCC
 CAAAGTGACCAAGACATAACAAAGACC**TAA**CAGTTGCAGATATGAGCTGTATAATT
 ATTATATATTAATAAAGAAGTTGCATTACCCCTCAAAAAAAAAAAAAAAA

FIGURE 86

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64902
><subunit 1 of 1, 451 aa, 1 stop
><MW: 49675, pI: 7.15, NX(S/T): 1
MVPEVRVLSSILLGLALLWFPLDSHARARPDMFCLFHGKRYSPGESWHPYLEPQGLMYCLRCT
CSEGAHVSCYRLHCPPVHCPQPVTEPQQCCPKCVEPHTPSGLRAPPKSCQHNGTMYQHGEIF
SAHELFPSRLPNQCVLCSTEGQIYCGLTTCPEPGCPAPLPLPDSCCQACKDEASEQSDEED
SVQSLHGVRHPQDPCSSDAGRKRGPGT PAPTGLSAPLSFI PRHFRPKGAGSTTVKIVLKEKH
KKACVHGGKTYSHGEVWHPAFRAFGPLPCILCTCEDGRQDCQRVTCPT EYPCRHPEKVAGKC
CKICPEDKADPGHSEISSSTRCPKAPGRVLVHTSVSPSPDNLRRFALEHEASDLVEIYLWKLV
KDEETEAQRGEVPGPRPHSQNLPLSDQESQEARLPERGTALPTARWPPRRSLERLPSPDPG
AEGHGQSRQSDQDITKT
```

Signal peptide:

amino acids 1-25

FIGURE 87

CTAGCCTGCGCCAAGGGGTAGTGAGACCGCGCGGCAACAGCTTGCCTGGCTGCCGGAGCTCCC
GTGGCGCTCCGCTGGCTGTGCAGGGCC**ATGG**TTCCTGCGGAAAATGCTGATCTCAGT
CGCAATGCTGGCGCAGGGCTGGCGTGGCTACCGCTCCTCGTTATCGTACCCCGGGAG
AGCGGCCGAAGCAGGAAATGCTAAAGGAGATGCCACTGCAGGACCAAGGAGCAGGGAGGAG
GCGGCCAGGACCCAGCAGCTATTGCTGGCCACTCTGCAGGAGGCAGCGACCACGCAGGAGAA
CGTGGCCTGGAGGAAGAAGTGGATGGTGGCGCGAAGGCGGCCAGCGGGAGGTACCGT**T**
GAACCGGACTTGCCTCCGTGGCGCCGGACCTTGGCTGGCGCAGGAATCCGAGGCAGCC
TTTCTCCTCGTGGGCCAGCGGAGAGTCCGGACCGAGATAACCATGCCAGGACTCTCCGGGG
TCCTGTGAGCTGCCGTGGGTGAGCACGTTCCCCAAACCCCTGGACTGACTGCTTAAGGT
CCGCAAGGCGGCCAGGCCAGACCGAGTCGGATGTGGTGAAGTGAACCAATAAAA
TCATGTTCCCTCAAAAAAAAAAAAAAAA
AAAAAAAAAAA

FIGURE 88

MDSLRKMLISVAMLGAGAGVGYALLVIVTPGERRKQEMLKEMPLQDPRSREEAARTQQLLA
TLQEAAATTQENVAWRKNWMVGEGGASGRSP

Signal peptide:

amino acids 1-18

FIGURE 89

CAGGAGAGAAGGCACGCCCCACCCCGCTCCAAAGCTAACCTCGGGCTTGAGGGGAAGA
 GGCTGACTGTACGTTCTTCACTCTGGCACCCTCTCCAGGCTGCC**ATGGGGCC**CAGCACC
 CCTCTCCTCATCTTGTCTTGTCTGGTCGGGACCCCTCCAAGGACAGCAGCACCACCT
 TGTGGAGTACATGGAACGCCGACTAGCTGCTTAGAGGAACGGCTGGCCAGTGCCAGGACC
 AGAGTAGTCGGCATGCTGCTGAGCTGCGGGACTTCAAGAACAAAGATGCTGCCACTGCTGGAG
 GTGGCAGAGAAGGAGCGGGAGGCACTCAGAACTGAGGCCACACCCTCCGGGAGAGTGGA
 TCGTCTGGAGCGGGAGGTAGACTATCTGGAGACCCAGAACCCAGCTCTGCCCTGTAGAGT
 TTGATGAGAAGGTGACTGGAGGCCCTGGGACCAAAGGCAAGGAAAGAAGGAATGAGAAGTAC
 GATATGGTACAGACTGTGGCTACACAATCTCAAGTGAGATCAATGAAGATTCTGAAGCG
 ATTTGGTGGCCCAGCTGGTCTATGGACCAAGGATCCACTGGGCAAACAGAGAAGATCTACG
 TGTTAGATGGACACAGAAATGACACAGCCTTGTCTCCCAAGGCTGCGTACTTCACCCCT
 GCCATGGCTGCCCGGAAAGCTCCCGAGTCGGGTGCCCTCCCTGGTAGGCACAGGGCA
 GCTGGTATATGGTGGCTTCTTATTTGCTCGGAGGCCTCCTGGAAGACACTGGTGGAGGTG
 GTGAGATGGAGAACACTTGCAGCTAACAAATTCCACCTGGCAAACCGAACAGTGGTGGAC
 AGCTCAGTATTCCAGCAGAGGGCTGATCCCCCCTACGGCTTGACAGCAGCACCTACAT
 CGACCTGGTAGCTGATGAGGAAGGTCTTGGCTGTCTATGCCACCCGGAGGATGACAGGC
 ACTTGTGTCTGGCCAAGTTAGATCCACAGACACTGGACACAGAGCAGCAGTGGACACACCA
 TGTCCCAGAGAGAATGCTGAGGCTGCCTTGTCTGTGGACCCCTATGTCGTCTATAA
 CACCCGTCCTGCCAGTCGGCCCGCATCCAGTGCTCCTTGATGCCAGCGCACCCGTACCC
 CTGAACGGGCAGCACTCCCTATTTCCCGCAGATATGGTGCCTATGCCAGCCTCCGCTAT
 AACCCCCGAGAACGCCAGCTATGCCCTGGGATGATGGCTACCGATTGTCTATAAGCTGGA
 GATGAGGAAGAAAGAGGGAGGAGGTT**TGAGGAGCTAGCCTGTTTG**CATCTTCTCACTC
 CCATACATTATATTATATCCCCACTAAATTCTTGTCTCATTCTCAAATGTGGGCCAG
 TTGTGGCTCAAATCCTCTATTTAGCCAATGGCAATCAAATTCTTCAGCTCCTTGTT
 TCATACGGAACTCCAGATCCTGAGTAATCCTTAGAGCCGAAGAGTCACAAACCCCTCAATG
 TTCCCTCCTGCTCTGCCCATGTCAACAAATTCAAGGCTAACCCAGACCCAGG
 GCTCTAACCTGTATGCCGGCAGGCCAGGGAGCAGGCAGCAGTGTCTCCCTCAGAGTG
 ACTTGGGAGGGAGAAATAGGAGGAGACGTCCAGCTGTCTCTTCACTCCTCCCT
 TCAGTGTCTGAGGAACAGGACTTCTCCACATTGTTGTATTGCAACATTGCAATTAAA
 AGGAAAATCCACAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 90

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64905
<subunit 1 of 1, 406 aa, 1 stop
<MW: 46038, pI: 6.50, NX(S/T): 2
MPGPSTPLLILFLLSGPLQGQQHHLVEYMERLAALERLAQCQDQSSRHAELRDFKNKM
LPLLEVAEKEREALRTEADTISGRVDRLEREVDYLETQNPALPCVEFDEKVTGGPGTKGKGR
RNEKYDMVTDCGYTISQVRSMKILKRFGGPAGLWTKDPLGQTEKIYVLDGTQNDTAFVFPR
RDFTLAMAARKASRVRVFPWVGTGQLVYGGFLYFARRPPGRPGGGEMENTLQLIKFHLAN
RTVVVDSSVFPAEGLIPPYGLTADTYIDLVADEEGLWAVYATREDDRHLCLAKLDPQTLDTEQ
QWDTPCPRENAAAFVICGTLYVVVNTRPASRARIQCSFDASGTLTPERAALPYFPRRYGAH
ASLRYNPRERQLYAWDDGYQIVYKLEMRKKEEEV
```

Important features:

Signal peptide:

amino acids 1-21

N-glycosylation sites.

amino acids 177-180, 248-251

FIGURE 91

GACAGCTGTCTCGATGGAGTAGACTCTCAGAACAGCGCAGTTGCCCTCCGCTCACGCAG
 AGCCTCTCCGGCTTCCGCACCTTGAGCATTAGGCCAGTCTCCTCTCTCTAATCCAT
 CCGTCACCTCTCCTGTCATCCGTTCCATGCCGTGAGGTCCATTACAGAACACAT**CCATGG**
 CTCTCATGCTCAGTTGGTTCTGAGTCTCCTCAAGCTGGGATCAGGGCAGTGGCAGGTGTT
 GGGCCAGACAAGCCTGTCCAGGCCTGGTGGGGAGGACGCAGCATTCTCCTGTTCCGTGTC
 TCCTAAGACCAATGCAGAGGCCATGGAAGTGCAGGTTCTCAGGGCCAGTCTCTAGCGTGG
 TCCACCTCTACAGGGACGGGAAGGACCAGCCATTATGCAGATGCCACAGTATCAAGGCAGG
 ACAAAACTGGTGAAGGATTCTATTGCGGAGGGCGCATCTCTTGAGGCTGGAAAACATTAC
 TGTGTGGATGCTGGCCTCTATGGGTGCAGGATTAGTCCCAGTCTTACTACCAGAAGGCCA
 TCTGGGAGCTACAGGTGTCAGCACTGGGCTCAGTTCTCTCATTCCATCACGGGATATGTT
 GATAGAGACATCCAGCTACTCTGTCAGTCCTCGGGCTGGTCCCCGGCCCACAGCGAAGTG
 GAAAGGTCCACAAGGACAGGATTGTCCACAGACTCCAGGACAAACAGAGACATGCATGGCC
 TGTTGATGTGGAGATCTCTGACCGTCCAAGAGAACGCCGGAGCATATCCTGTTCCATG
 CGGCATGCTCATCTGAGCCGAGAGGTGGAATCCAGGGTACAGATAGGAGATACTTTTCGA
 GCCTATATCGTGGCACCTGGCTACCAAAGTACTGGAAACTCTGCTGTGGCCTATTTTG
 GCATTGTTGGACTGAAGATTTCTTCTCAAATTCCAGTGGAAAATCCAGGCGGAACGGAC
 TGGAGAAGAAAGCACGGACAGGCAGAATTGAGAGACGCCGGAAACACGCAGTGGAGGTGAC
 TCTGGATCCAGAGACGGCTACCCGAAGCTCTGCGTTCTGATCTGAAAATGTAACCCATA
 GAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAAGAGTGTGGTGGCT
 TCTCAGAGTTCCAAGCAGGGAAACATTACTGGGAGGTGGACGGAGGACACAATAAGGTG
 GCGCGTGGGAGTGTGCCGGATGATGTGGACAGGAGGAAGGAGTACGTGACTTGTCTCCG
 ATCATGGGTACTGGGTCTCAGACTGAATGGAGAACATTGTATTCACATTAAATCCCCGT
 TTTATCAGCGTCTTCCCCAGGACCCCACCTACAAAAAATAGGGGTCTCCTGGACTATGAGTG
 TGGGACCACCTCCTTCTCAACATAATGACCAGTCCCTATTACCCCTGACATGTCGGT
 TTGAAGGCTTATTGAGGCCCTACATTGAGTATCCGTCCTATAATGAGCAAAATGGAACCTCC
 ATAGTCATCTGCCAGTCACCCAGGAATCAGAGAAAGAGGCCTTGGCAAAGGGCCTCTGC
 AATCCCAGAGACAAGCAACAGTGAGTCCTCCTCACAGGCAACCACGCCCTCCCCAGGG
 GTGAAATG**TAG**GATGAATCACATCCCACATTCTTCTTAGGGATATTAGGTCTCTCCCA
 GATCCAAAGTCCCGCAGCAGCCGCCAAGGTGGCTCAGATGAAGGGGACTGGCCTGTCC
 ACATGGGAGTCAGGTGTATGGCTGCCCTGAGCTGGAGGGAAAGAAGGCTGACATTACATT
 AGTTGCTCTCACTCCATCTGGCTAAGTGATCTTGAAATACCACCTCTCAGGTGAAGAACCG
 TCAGGAATTCCCATCTCACAGGCTGTGGTAGATTAAGTAGACAAGGAATGTGAATAATGC
 TTAGATCTTATTGATGACAGAGTGTATCCTAATGGTTGTTCAATTATATTACACTTCA
 AAAAAA

FIGURE 92

MALMLSLVLSLLKLGSGQWQVFGPDKPVQALVGEDAASFCLSPKTNAEAMEVRFFRGQFSS
VVHLYRDGKDQPFMQMPOYQGRTKLVKDSIAEGRISLRLENITVLDAGLYGCRISSQSYYQK
AIWELQVSALGSVP LISITGYVDRDIQLLCQSSGWFPRPTAKWKGPQGQDLSTDRTNRDMH
GLFDVEISLTQENAGSISCSMRHAHLSREVESRVQIGDTFFEPISWHLATKVLGILCCGLF
FGIVGLKIFFSKFQWKIQAELDWRRKHGQAEELRDARKHAVEVTLDPETAHPKLCSVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVASQSFQAGKHYWEVDGGHNKRWRVGVCRDDVDRRKEYVTL
PDHGYWVLRLNGEHLYFTLNPRFISVFPRTPPTKIGVFLDYECGTISFFNINDQSLIYTLTC
RFEGLLRPYIEYPSYNEQNGTPIVICPVTQESEKEASWQRASAI PETSNSESSSQATTPFLP
RGEM

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 239-255

FIGURE 93

GCGATGGTGCCTGGCGGTGGCGGGCGTTGCGGAGGCTTCCTGGTCGGATTGCA
 ACGAGGAGAAGATGACTGACCAACCAGCTGGCTGAATGAATGAATGGCGGAGCCGAGCGC
CATGAGGAGCCTGCCGAGCCTGGCGGCCTCGCCCTGTTGTGCTGCGCCGCCGCCGCC
 CCGTCGCCTCAGCCGCCTCGGCGGGGAATGTCACCGGTGGCGGGGCCGCCGCC
 GACGCGTCGCCGGGCCCCGGGTTGCGGGCGAGCCCAGCCACCCCTCCCTAGGGCGACGGC
 TCCACGGCCCAGGCCCCGAGGACCGGGCCCCCGCGCCACCGTCCACCGAACCCCTGGCTG
 CGACTTCTCCAGCCCAGTCCCCGGAGACCAACCCCTTTGGCGACTGCTGGACCCCTTCC
 ACCACCTTCAAGCGCCGCTGCCGCCCTCGCCGACCACCCCTCCGGCGGCCGAACGCACTTC
 GACCACCTCTCAGGCGCCGACCAGACCCCGCGCCGACCACCCCTTGACGACCACGGCCCG
 CGCCGACCACCCCTGTAGCACCACCGTACCGGCCACAGACTCCCCGGACCCCGACCCCC
 GATCTCCCCAGCAGCAGCAACAGCAGCGTCCTCCCCACCCACCTGCCACCGAGGCCCCCTC
 TTCGCCTCTCCAGAGTATGTAACTGCTCTGTGGTTGAAGCTGAATGTGAATCGCT
 GCAACCAGACCAACAGGGCAGTGTGAGTGTGGCCAGGTTACAGGGGCTTCACTGTGAAACC
 TGCAAAGAGGGCTTTACCTAAATTACACTTCTGGGCTCTGTCAGCCATGTGACTGTAGTCC
 ACATGGAGCTCTCAGCATACCGTGCAACAGG**TAA**GAACAGAGGGTGGAACTGAAGTTATT
 TTATTTAGCAAGGGAAAAAAAAGGCTGCTACTCTCAAGGACCATACTGGTTAAACAAAG
 GAGGATGAGGGTCATAGATTACAAAATATTTATATACTTTATTCTCTTACTTATATGT
 TATATTAATGTCAGGATTAAACATCTAATTACTGATTTAGTTCTTCAAAAGCACTAG
 AGTCGCCAATTTCCTGGATAATTCTGTAAATTCTCATGGGAAAAATTATTGAAGAAT
 AAATCTGCTTCTGGAGGGCTTCAGGCATGAAACCTGCTAGGAGGTTAGAAATGTTCT
 ATGTTATTAATATACCATTGGAGTTGAGGAAATTGTTGTTGGTTATTCTCTCTA
 ATCAAAATTCTACATTGTTCTTGGACATCTAAAGCTAACCTGGGGTACCTAATT
 TTTAACTAGTGGTAAGTAGACTGGTTTACTCTATTACAGTACATTGAGACCAAAAG
 TAGATTAAGCAGGAATTATCTTAAACTATTATGTTATTGGAGGTAATTAAATCTAGTGG
 ATAATGTAAGTGTATCTAACGATTGCTTGTACTGCACGAAAGTAATTATTCTTGACCT
 TATGTGAGGCACCTGGCTTTGTGGACCCCAAGTCAAAAAACTGAAGAGACAGTATTAAAT
 AATGAAAAAAATAATGACAGGTTAACTCAGTGTAAACCTGGGTATAACCCAAAGATCTGCTGC
 CACTTACGAGCTGTGTTCTGGCAAGTAATTCTTCACTGAGCTGTTCTCAAG
 GTTGTGTGAAGATTAATGAGTTGATATATAAAATGCCAGCACATGTCACTCAATAAA
 TTCTGGTTGTTAAATTCTAAAGGAATATTATGAGCTGAAATGAGAGAACATGTTAAAGA
 ACTTTAGCTCCTGACAAAGAAGTGTCTTATACTTTAGCACTAAATATTTAAATGCTTTA
 TAAATGATATTATACTGTTATGGAATATTGTATCATATTGTAGTTATTAAAAATGTAGAAG
 AGGCTGGCGCGGTGGCTCACGCCGTAAATCCTAGCAGCTTGGGAGGCCAGGGGGTGGAT
 CACTTGAGGCCAGGAGTTCTAGATGAGCTGGCCAGCACAGTGAACCCCCGCTCTACTAAA
 AATACAAACAAATTAGCTGGCGTGGTGGCACACACCTGTAGTCCCAGCTACTGGGAGGCT
 GAGGCAGGAGAATCGGTGAACCCGGGAGGTGGAGGTTGCAGTGAGCTGAGATCGGCCACT
 GCACTCCAGCCTGGTGAAGAGAGGGAGACTCTGTCTAAAAAAAAAAAAAA

FIGURE 94

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA64952
><subunit 1 of 1, 258 aa, 1 stop
><MW: 25716, pI: 8.13, NX(S/T): 5
MRSLPSLGGALLCCAAAAAVASAASAGNVTGGGAAGQVDASPGPGLRGEPSHPFPRATA
PTAQAPRTGPPRATVHRPLAATSPAQSPEPPPLWATAGPSSTTFQAPLGPSPTTPPAAERTS
TTSQAPTRPAPTLSTTGAPPTPVATTVPAPTPRTPTPDLPSSNSSVLPTPPATEAPS
SPPPEYVCNCNVGSILNVNRCNQTTGQCECRPGYQGLHCETCKEGFYLNYSGLCQPCDCSP
HGALSIPCNR
```

Important features of the protein:

Signal peptide:

amino acids 1-25

N-glycosylation sites.

amino acids 30-33, 172-175, 195-198, 208-211, 235-238

EGF-like domain cysteine pattern signature.

amino acids 214-226.

FIGURE 95

TGCGGCGCAGTGTAGACCTGGGAGGATGGGCGGCCTGCTGCTGGCTGCTTTCTGGCTTG
TCTCGGTGCCAGGGCCCAGGCCGTGTGGTGGAAAGACTGGACCCTGAGCAGCTTCTGG
CCCTGGTACGTGCTTGCCTGGCTCCCGGAAAAGGGCTTGCCATGGAGAAGGACATGAA
GAACGTCGTGGGGTGGTGGTGGACCTCACTCCAGAAAACAACCTGCGGACGCTGTCCCTCTC
AGCACGGCTGGGAGGGTGTGACCAGAGTGTATGGACCTGATAAAGCGAAACTCCGGATGG
GTGTTGAGAATCCCTCAATAGCGTGCTGGAGCTCTGGTGCTGCCACCAACTCAGAGA
CTATGCCATCATCTTCACTCAGCTGGAGTCGGGGACGAGCCCTCAACACCGTGGAGCTGT
ACAGTCTGACGGAGACAGCCAGGCCAGGAGGCCATGGGCTCTCACCAAGTGGAGCAGGAGC
CTGGGCTTCTGTACAGTAGCAGGCCAGCTGCAGAAGGACCTCACCTGTGCTACAAGAT
CCTTCTGTGAGTGCTGCGTCCCCAGTAGGGATGGCGCCACAGGGCCTGTGACCTCGGCCA
GTGTCCACCCACCTCGCTCAGCGGCTCCGGGGCCAGCACAGCTCAGAATAAAGCGATT
CACAGCA

FIGURE 96

MGGLLLAFLALVSVPRAQAVWLGRLDPEQLLGPWYVLAVASREKGFAMEKDMKNVVGVVVT
LTPENNLRLLSQHGLGGCDQSVMIDLIKRNSGWVFENPSIGVLELWVLATNFRDYAIIFTQL
EFGDEPFNTVELYSLTETASQEAMGLFTKWSRSLGFLSQ

Signal peptide:

amino acids 1-20

FIGURE 97

AACAGACGTTCCCTCGCGGCCCTGGCACCTCTAACCCCAGACATGCTGCTGCTGCTGCTGCC
 CCTGCTCTGGGGGAGGGAGAGGGCGGAAGGACAGACAAGTAAACTGCTGACGATGCAGAGTT
 CCGTGACGGTGCAGGAAGGCCTGTGTCCATGTGCCCTGCTCCTCTCCTACCCCTCGCAT
 GGCTGGATTACCCCTGGCCAGTAGTTCATGGCTACTGGTCCGGGAAGGGCCAATACAGA
 CCAGGATGCTCCAGTGGCCACAAACAACCCAGCTGGCAGTGTGGGAGGAGACTGGGACC
 GATTCCACCTCCTGGGACCCACATACCAAGAATTGCACCCCTGAGCAGATGCCAGA
 AGAAGTGATGCGGGGAGATACTTCTTCGTATGGAGAAAGGAAGTATAAAATGGAATTATAA
 ACATCACCGGCTCTGTGAATGTGACAGCCTGACCCACAGGCCAACATCCTCATCCCAG
 GCACCCCTGGAGTCCGGCTGCCCTCAGAATCTGACCTGCTCTGTGCCCTGGCCTGTGAGCAG
 GGGACACCCCCATGATCTCCTGGATAGGGACCTCCGTGTCCCCCTGGACCCCTCCACCAC
 CCGCTCCTCGGTGCTACCCCTATCCCACAGCCCCAGGACCATGGCACCCACGCTCACCTGTC
 AGGTGACCTTCCCTGGGCCAGCGTGACCACGAACAAGACCGTCCATCTAACGTGTCTAC
 CCGCCTCAGAACTTGACCATGACTGTCTTCCAAGGAGACGGCACAGTATCCACAGTCTGGG
 AAATGGCTCATCTCTGTCACTCCCAGAGGGCCAGTCTCTGCGCCTGGTCTGTGAGTTGATG
 CAGTTGACAGCAATCCCCCTGCCAGGCTGAGCCTGAGCTGGAGAGGCCTGACCCCTGTGCC
 TCACAGCCCTCAAACCCCCGGGTGCTGGAGCTGCCCTGGTGCACCTGAGGGATGCAGCTGA
 ATTACCTGCAGAGCTCAGAACCCCTCAGCAGGTCTACCTGAACGTCTCCCTGC
 AGAGCAAAGCCACATCAGGAGTGACTCAGGGGGTGGTCGGGGAGCTGGAGCCACAGCC
 GTCTTCCCTGTCCTCTGCGTCATCTCGTTGAGGTCCCTGCAGGAAGAAATCGGCAAG
 GCCAGCAGCGGGCGTGGGAGATA CGGGCATAGAGGATGCAAACGCTGTCAGGGTTCA
 CTCAGGGGCCCTGACTGAACCTTGGCAGAACAGACAGTCCCCAGACCAGCCTCCCCAGCT
 TCTGCCGCTCCTCAGTGGGGAGGGAGAGCTCCAGTATGCATCCCTCAGCTCCAGATGGT
 GAAGCCTTGGACTCGCGGGGACAGGAGGCCACTGACACCGAGTACTCGGAGATCAAGATCC
 ACAGATGAGAAACTGCAGAGACTCACCTGATTGAGGGATCACAGCCCTCCAGGAAGGGA
 GAAGTCAGAGGGCTGATTCTGTAGAATTAAACAGCCCTAACGTGATGAGCTATGATAACACT
 ATGAATTATGTGCAGAGTGAAAAGCACACAGGTTAGAGTCAAAGTATCTCAAACCTGAAT
 CCACACTGTGCCCTCCCTTTATTTTTAACTAAAAGACAGACAAATTCCCTA

FIGURE 98

MLLLLLPLLWGRERAEGQTSKLLTMQSSVTVQEGLCVHVPSCFSYPSHGWIYPGPVVHGYWF
REGANTDQDAPVATNNPARAVWEETRDRFHLLGDPHTKNCTL SIRDARRSDAGRYFFRMEKG
SIKWNYKHHRLSVNVTALTHRPNILIPGTLESGCPQNLTCSVPWACEQGTPPMISWIGTSVS
PLDPSTTRSSVLTLPQPQDHGTSLTCQVTFPGASVTTNKTVHLNVSYPPQNLTMVFQGDG
TVSTVLGNSSLSLPEGQSLRLVCAVDADSNPPARLSLSWRGLTLCPSQPSNPGVLELPWV
HLRDAAEFTCRAQNPLGSQQVYLNVS LQSKATSGVTQGVVGGAGATALVFLSFCVIFVVVR
CRKK SARPAAGVGDTGIEDANAVRG SASQGPLTEPWAEDSPPDQPPPASARSSVGEGELOYA
SLSFQMVKPWDSRGQEATDTEYSEIKIHR

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 351-370

FIGURE 99

卷之三

FIGURE 100

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65404
<subunit 1 of 1, 170 aa, 1 stop
<MW: 19457, pI: 9.10, NX(S/T): 0
MKTLFLGVTLGLAAALSLTLEEDITGTWYVKAMVVDKDFPEDRRPRKVSPVKVTALGGGKL
EATFTFMREDRCIQKKILMRKTEEPGKYSAYGGRKLMYLQELPRRDHYIFYCKDQHHGGLLH
MGKLVGRNSDTNREALEEFKKLVQRKGLSEEDIFTPLQTGSCVPEH
```

Important features:

Signal peptide:

amino acids 1-17

FIGURE 101

GTTCCGCAGATGCAGAGGTTGAGGTGGCTGCGGGACTGGAAGTCATCGGGCAGAGGTCTCAC
 AGCAGCCAAGGAACCTGGGGCCCGCTCCTCCCCCTCCAGGCC **ATG**AGGATTCTGCAGTTAA
 TCCTGCTTGCCTGGCAACAGGGCTTGTAGGGGGAGAGACCAGGATCATCAAGGGGTTGAG
 TGCAAGCCTCACTCCCAGCCCTGGCAGGCAGCCCTGTTGAGAAGACGCGGCTACTCTGTGG
 GGCAGCAGCTCATGCCCGAGATGGCTCCTGACAGCAGCCCAGTGCCTCAAGCCCCGCTACA
 TAGTTCACCTGGGCAGCACAACCTCCAGAAGGAGGAGGGCTGTGAGCAGACCCGGACAGCC
 ACTGAGTCCTCCCCACCCCGGCTCAACAAACAGCCTCCCCAACAAAGACCACCGCAATGA
 CATCATGCTGGTGAAGATGGCATGCCAGTCTCCATCACCTGGCTGTGCGACCCCTCACCC
 TCTCCTCACGCTGTGTCAGTGGCACCAGCTGCCCTATTCCGGCTGGGGCAGCACGTCC
 AGCCCCCAGTTACGCCTGCCTCACACCTTGCATGCCAACATCACCATTGAGCACCA
 GAAGTGTGAGAACGCCTACCCGGCAACATCACAGACACCATTGGTGTGCCAGCGTGCAGG
 AAGGGGGCAAGGACTCCTGCCAGGGTGACTCCGGGGCCCTCTGGTCTGTAACCAGTCTTT
 CAAGGCATTATCTCCTGGGCCAGGATCCGTGTGCGATCACCGAAAGCCTGGTGTACAC
 GAAAGTCTGCAAATATGTGGACTGGATCCAGGAGACGATGAAGAACAAAT**TAG**ACTGGACCCA
 CCCACCACAGCCCATTCCACCTTCCACTGGTGTGTTGGTCTGTTCACTCTGTTAAT
 AAGAAAACCTAACGCAAGACCCCTACGAACATTCTTGGGCTCCTGGACTACAGGAGATG
 CTGTCACTTAATAATCAACCTGGGTTGAAATCAGTGAGACCTGGATTCAAATTCTGCCCT
 GAAATATTGTGACTCTGGGAATGACAACACCTGGTTGTTCTGTTGTATCCCCAGCCCCA
 AAGACAGCTCCTGGCCATATCAAGGTTCAATAAATATTGCTAAATGAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 102

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65405
<subunit 1 of 1, 250 aa, 1 stop
<MW: 27466, pI: 8.87, NX(S/T): 4
MRILQLILLALATGLVGGETRIIKGFECKPHSQWPQAALFEKTRLLCGATLIAPRWLLAAH
CLKPRYIVHLGQHNLQKEEGCEQRTATESFPHPGFNNSLPNKDHRNDIMLVKMASPVSITW
AVRPLTLSSRCVTAGTSCLISGWGSTSSPQLRLPHTLRCANITIIIEHQKCENAYPGNITDTM
VCASVQEGGKDSCQGDGGPLVCNQSLQGIISWGQDPCAITRKPGVYTKVCKYVDWIQETMKNN
```

Important features:

Signal peptide:

amino acids 1-18

Serine proteases, trypsin family, histidine active site.

amino acids 58-63

N-glycosylation sites.

amino acids 99-102, 165-168, 181-184, 210-213

Glycosaminoglycan attachment site.

amino acids 145-148

Kringle domain proteins.

amino acids 197-209, 47-64

Serine proteases, trypsin family, histidine protein

amino acids 199-209, 47-63, 220-243

Apple domain proteins

amino acids 222-249, 189-222

FIGURE 103

FIGURE 104

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA65406
<subunit 1 of 1, 222 aa, 1 stop
<MW: 25794, pI: 6.24, NX(S/T): 1
MPKTMHFLFRFIVFFYLWGLFTAQRQKKEESTEEVKIEVLHRPENCSKTSKKGDLLNAHYDG
YLAKDGSKFYCSRTQNEGHPKWFVLGVGQVIKGLDIAMTDMCPGEKRKVVIIPPSFAYGKEGY
AEGKIPPDATLIFEIELYAVTKGPRSIETFKQIDMDNDRQLSKAEINLYLQREFEKDEKPRD
KSYQDAVLEDIFKKNDHDGDGFISPKEYNVYQHDEL
```

Important features:

Endoplasmic reticulum targeting sequence.

amino acids 219-222

N-glycosylation site.

amino acids 45-48

FKBP-type peptidyl-prolyl cis-trans isomerase

amino acids 87-223, 129-142

EF-hand calcium-binding domain proteins

amino acids 202-214, 195-214

FIGURE 105

CAGAA**ATG**CAGGGACCATTGCTTCTTCAGGCCTCTGCTTCTGCTGAGCCTCTTGGAGCT
GTGACTCAGAAAACCAAAACTTCCTGTGCTAAGTGCCCCCAAATGCTTCCTGTGTCAATAA
CACTCACTGCACCTGCAACCATGGATATACTTCTGGATCTGGCAGAAACTATTCACATTCC
CCTTGGAGACATGTAACGCCAGGCATGGTGGCTCGCGCCTG**TAA**TCCCAGTTCTTGGGAAG
CCAAGGCAGGTGGATCACCTGAGGTCAAGGAGTTGAGACCAGCCTGCCAACATAGTGAAC
CCCGTGTCTACTAAAAATACAAAAATCAGCCGGCGTGGTGGTGCATGCCTGCAATCCAGT
TACTCGGGAGGCTGAGGCAGGAGAATCGCTGAACTCAGGAGGCAGAAGTTGCAGTGAACCC
AGATCCTGCCATTGCACTCCAGCATGGATGACAGAGCAAGACTCCGTCTCAAAAAGAAAAGA
TAGTTCTTGTTCATTCGCGACTGCCCTCTCAGTGTTCCTGGATCCCCTCCAAATAA
AGTACTTATATTCTC

FIGURE 106

MQGPLLLPGLCFLSLFGAVTQKTAKCAPPNASCVNNTHCTCNHGYTSGSGQKLFTFPL
ETCNARHGGSR

Signal peptide:

amino acids 1-18

FIGURE 107

CAAGCAGGTCACTCCCTGGTACCTCAAAGAGAAGCAGAGAGGGCAGAGGTGGGGGCAC
 AGGGAAAGGGT GACCTCTGAGATTCCCCTTTCCCCAGACTTGGAAAGTGACCCACC**ATGG**
 GGCTCAGCATTTTGCTCCTGTGTGTTCTGGGCTCAGCCAGGCAGCCACACCGAAGATT
 TTCAATGGCACTGAGTGTGGCGTAACTCACAGCCGTGGCAGGTGGGGCTGTTGAGGGCAC
 CAGCCTGCGCTCGGGGGTGCCTTATTGACCACAGGTGGTCCTCACAGCGGCTCACTGCA
 CGGGCAGCAGGTACTGGGTGCGCCTGGGGAACACACAGCCTCAGCCAGCTCGACTGGACCGAG
 CAGATCCGGCACAGCGGTTCTGTGACCCATCCGGTACCTGGGAGCCTCGACGAGCCA
 CGAGCACGACCTCCGGCTGCTGCGGCTGCCGTCCCGTAACCAGCAGCGTTAAC
 CCCTGCCCTGCCAATGACTGTGCAACCGCTGGCACCGAGTGCCACGTCTCAGGCTGGGC
 ATCACCAACCACCCACGGAACCCATTCCGGATCTGCTCCAGTGCCCTAACCTCTCCATCGT
 CTCCCATGCCACCTGCCATGGTGTGTATCCCGGGAGAATCACGAGCAACATGGTGTGTGCAG
 GCGGCGTCCCAGGATGCCAGGGTATTCTGGGGCCCTGGTGTGTGGGA
 GTCCTCAAGGTCTGGTGCCTGGGGTCTGTGGGCCCTGTGGACAAGATGGCATCCCTGG
 AGTCTACACCTATTTGCAAGTATGTGGACTGGATCCGGATGATCATGAGGAAC**TGA**C
 CTGTTCCCTCACCTCCACCCCCACCCCTAACCTGGTACCCCTCTGGCCCTCAGAGCACC
 AATATCTCCTCCATCACTCCCTAGCTCCACTCTTGGTGGCCTGGAACTTCTGGAACTT
 TAACTCCTGCCAGCCCTCTAAGACCCACGAGCGGGTGAGAGAAGTGTGCAATAGTCTGGA
 ATAAAATATAATGAAGGAGGGCAAAAAAAA

FIGURE 108

MGLSIFLLLGVLSQAATPKIFNGTECGRNSQPWQVGLFEGTSLRCGGVLIDHRWVLTAAC
CSGSRYWVRLGEHSLSQLDWTEQIRHSGFSVTHPGYLGASTSHEHDLRLLRLRLPVRVTSSV
QPLPLPNDCATAGTECHVSGWGITNHPRNPFPDLLQCLNLSIVSHATCHGVYPGRITSNMVC
AGGVPGQDACQGDGGPLVCGGVLQGLVSWGSVGPGCQDGIPGVYTYICKYVDWIRMIMRNN

Signal peptide:

amino acids 1-17

FIGURE 109

GCGGCCACACG CAGCTAGCCGGAGCCC GGACCAGGC GCCTGTGCCTCCTCGTCCCTCGC
 CGCGTCCCGAAGCCTGGAGCCGGC GGGAGCCCCCGC GCTCGCC **ATGT** CGGGCGAGCTCAGCA
 ACAGGTTCCAAGGAGGGAAGGC GTTCGGCTTGCTCAAAGCCGGCAGGAGAGGAGGCTGGCC
 GAGATCAACC GGGAGTTCTGTGACCAAGTACAGTGATGAAGAGAACCTCCAGAAAAA
 GCTCACAGCCTCAAAGAGAA GTACATGGAGTTGACCTGAACAATGAAGGC GAGATTGACC
 TGATGTCTTAAAGAGGATGATGGAGAAGCTGGTGTCCCCAAGACCCAC TGGAGATGAAG
 AAGATGATCTCAGAGGTGACAGGAGGGT CAGTGACACTATATCCTACCGAGACTTGTGAA
 CATGATGCTGGGAAACGGT CGGCTGT CCTCAAGTTAGTCATGATGTTGAAGGAAAAGCCA
 ACGAGAGCAGCCCCAAGCCAGTTGGCCCCCTCCAGAGAGACATTGCTAGCCTGCCCT**TGA**
 GGACCCCGCCTGGACTCCCCAGCCTCCCACCCCATACCTCCCTCCGATCTGCTGCCCTT
 CTTGACACACTGTGATCTCTCTCTCATTTGTTGGTCATTGAGGGTTTGTGTT
 TCATCAATGTCTTGTAAAGCACAAATTATCTGCCTAAAGGGCTCTGGTCGGGAATCC
 TGAGCCTTGGTCCCCTCCCTCTCTTCCCTCCCTCCCCGCTCCGTGCAGAAGGGCTG
 ATATCAAACCAAAA ACTAGAGGGGGCAGGCCAGGGCAGGGAGGCTTCCAGCCTGTGTTCCC
 CTCACTTGGAGGAACCAGCACTCTCCATCCTTCAGAAAGTCTCCAAGCCAAGTTCAGGCTC
 ACTGACCTGGCTCTGACGAGGACCCCAGGCCACTCTGAGAAGACCTGGAGTAGGGACAAGG
 CTGCAGGGCCTCTTCGGTTCCCTGGACAGTGCCATGGTCCAGTGCTCTGGTGTACCC
 AGGACACAGCCACTCGGGCCCCGCTGCCCACTGATCCCACACTCATTCCACACCTCTTCT
 CATCCTCAGTGATGTGAAGGTGGAAAGGAAAGGAGCTGGCATTGGAGCCCTCAAGAAGG
 TACCAGAAGGAACCCCTCCAGTCCTGCTCTGGCACACCTGTGCAGGCAGCTGAGAGGCAG
 CGTGCAGCCCTACTGTCCCTACTGGGGCAGCAGAGGGCTCGGAGGCAGAAGTGAGGCCTG
 GGGTTGGGGGAAAGGT CAGTCAGTGCTGTTCCACCTTTAGGGAGGATACTGAGGGGAC
 CAGGATGGAGAATGAGGAGTAAAATGCTCACGGCAAAGTCAGCAGCACTGGTAAGCCAAGA
 CTGAGAAATACAAGGTTGCTGTGACCCCAATCTGCTGAAAAAAAAAAAAAAA

FIGURE 110

MSGELSNRFQGGKAFGLLKARQERRLAEINREFLCDQKYSDDEENLPEKLTAFKEKYMEFDLN
NEGEIDLMSLKRMMEKLGVPKTHLEMKKMISEVTGGVSDTISYRDFVNMMLGKRSAVLKVM
MFEGKANESSPKPVGPPPEDIASLP

FIGURE 111A

CGCGCTCCCCGCGCCTCCGGGCTCCACGCGTCTGCCCGCAGAGGCAGGCCCTCCA
 GGAGCGGGGCCCTGCACACC**ATGCCCCCGGTGGCAGGGT**CAGGCCGCGCC
 CGCCTGGCGCTGGCTGGCGACTGGCTGAGTGGCCTCCAGCCGTGCCCTGCC
 CACCAAGTGTACCTGCTCCGCTGCCAGCGTGGACTGCCACGGCTGGCCTCCGCGGGTT
 CTCGGGGCATCCCCGCAACGCTGAGCGCCTTGACCTGGACAGAAATAATACCAAGGATC
 ACCAAGATGGACTTCGCTGGCTCAAGAACCTCCGAGTCTTGATCTGAAGAGACAACCAGGT
 CAGCGTCATCGAGAGAGGGCGCTTCCAGGACCTGAAGCAGCTAGAGCGACTGCCCTGAACA
 AGAATAAGCTGCAAGTCCTCCAGAATTGCTTCCAGAGCACGCCAGCTCACCAAGACTA
 GATTTGAGTGAACCAACAGATCCAGGGATCCGAGGAAGGCCTCCGCGGCATCACCGATGT
 GAAGAACCTGCAACTGGACAACAAACACATCAGCTGCATTGAAGATGGAGCCTCCGAGCGC
 TGCAGCTGGAGATCCTTACCCCTAACAAACAACATCAGTCGATCCTGGTACCAAGC
 TTCAACCACATGCCGAAGATCCGAACCTGCGCCTCCACTCCAACCAACCTCTACTGCGACTG
 CCACCTGGCTCTGGATTGGCTGCAGCGACAGGACAGTTGCCAGTTCACACTCT
 GCATGGCTCTGTGCATTGAGGGCTTCAACGTGGCGATGTGCAGAAGAAGGAGTACGTG
 TGCCCAGCCCCCACTCGGAGCCCCATCCTGCAATGCCAACCTCCATCTGCCCTCGCC
 CTGCACGTGCAGCAATAACATCGTGGACTGTCGAGGAAAGGGCTGATGGAGATTCCCTGCCA
 ACTGCCGGAGGGCATCGCAAATAACGCTTAGAACAGAACCTCCATCAAAGCCATCCCTGCA
 GGAGCCTTCACCCAGTACAAGAAACTGAAGCGAATAGACATCAGCAAGAATCAGATATCGGA
 TATTGCTCCAGATGCCTTCCAGGGCTGAAATCACTCACATCGCTGGTCTGTATGGAAACA
 AGATCACCGAGATTGCCAAGGGACTGTTGATGGCTGGTCCCTACAGCTGCTCCTCTC
 AATGCCAACAGATCAACTGCCCTGGGTGAACACGTTTCAAGGACCTGCAGAACCTCAACTT
 GCTCTCCCTGTATGACAACAAAGCTGCAGACCATCAGCAAGGGCTCTCGCCCCCTGCACT
 CCATCCAGACACTCCACTTAGCCAAAACCCATTGTGTGCGACTGCCACTTGAAAGTGGCTG
 GCGCACTACCTCCAGGACAACCCATCGAGACAAGCGGGCCGCTGCAGCAGCCGCGCCG
 ACTGCCAACAGCGCATGCCAGATCAAGAGCAAGAAGTCCGCTGCTCAGGCTCCGAGG
 ATTACCGCAGCAGGTTCAGCAGCGAGTGCTCATGGACCTCGTGTGCCCGAGAAAGTGTGCG
 TGTGAGGGCACGATTGTGACTGCTCAACCAGAACAGCTGGTCCGCATCCAACGCCACCTCCC
 TGAATATGTCACCGACCTGCGACTGAATGACAATGAGGTATCTGTTCTGGAGGCCACTGGCA
 TCTTCAAGAACGTTGCCAACCTGCGGAAATAATGAGTAACAATAAGATCAAGGAGGTG
 CGAGAGGGAGCTTCGATGGAGCAGCCAGCGTGCAGGAGCTGATGCTGACAGGGAACAGCT
 GGAGACCGTGCACGGCGCGTGTCCGTCAGTGGCCTCAAAACCTTGATGCTGAGGA
 GTAACTGATCAGCTGTGAGTAATGACACCTTGCCGGCTGAGTCGGTGAGACTGCTG
 TCCCTCTATGACAATCGGATCACCACCATACCCCTGGGCCTTACCCACGCTTGTCTCC
 GTCCACCATAAACCTCTGTCCAACCCCTCAACTGCAACTGCCACCTGGCCTGGCTGGCA
 AGTGGTTGAGGAAGAGGGGATCGTCAGTGGAACCCCTAGGTGCCAGAACCCATTTC
 AAGGAGATTCCCATTCCAGGATGTGGCATCCAGGACTTCACCTGTGATGGCAACGAGGAGAG
 TAGCTGCCAGCTGAGCCCGCTGCCGGAGCAGTGCACCTGTATGGAGACAGTGGTGCGAT
 GCAGCAACAAGGGCTCCGCCCCCTCCAGAGGCATGCCAAGGATGTGACCGAGCTGTAC
 CTGGAAGGAAACCACTAACAGCCGTGCCAGAGAGACTGTCCGCCCTCCGACACCTGACGCT
 TATTGACCTGAGCAACACAGCATCAGCATGCTGACCAATTACACCTTCACTAACATGCTC
 ACCTCTCCACTCTGATCCTGAGCTACAACCGGCTGAGGTGCATCCCCGTCACGCCCTAAC
 GGGCTGCCGTCCCTGCGAGTGCTAACCTCCATGGCAATGACATTCCAGCGTCTGAAGG
 CTCCTCAACGACCTCACATCTTCCATCTGGCGCTGGGAACCAACCCACTCCACTGTG
 ACTGCAGTCTCGGTGGCTGCGAGTGGGTGAAGGGGGTACAAGGAGCCTGGCATGCC
 CGCTGCAGTAGCCCTGAGGCCATGGCTGACAGGCTCTGCTCACCACCCAAACCCACCGCTT
 CCAGTGCACAGGGCCAGTGGACATCAACATTGTGGCAAATGCAATGCCCTGCCAGCC
 CGTGCACAGAACGGACATGCACCCAGGACCTGTGGAGCTGTACCGCTGTGCCCTGCC

FIGURE 111B

TACAGCTACAAGGGCAAGGACTGCACTGTGCCCATCAACACCTGCATCCAGAACCCCTGTCA
 GCATGGAGGCACCTGCCACCTGAGTGACAGCCACAAGGATGGGTCAGCTGCTCCTGCCCTC
 TGGGCTTGAGGGCAGCGGTGTGAGATCAACCCAGATGACTGTGAGGACAACGACTGCGAA
 AACAAATGCCACCTGCGTGGACGGGATCAACAACACTACGTGTATCTGTCGCCCTA
 AGGTGAGCTATGCGACGAGGTGATTGACCCTGTGTGCCTGAGCTGAACCTCTGTCAGCATG
 AGGCCAAGTGCATCCCCCTGGACAAAGGATTCACTGAGCTGCAGTGTGTCCTGGCTACAGCGGG
 AAGCTCTGTGAGACAGACAATGATGACTGTGTGGCCCACAAGTGCCGCCACGGGGCCAGTG
 CGTGGACACAATCAATGGCTACACATGCACCTGCCCTCAGGCTTCAGTGGACCCCTGTG
 AACACCCCCCACCCATGGCCTACTGCAGACCAGCCATGCAGACCAGTACGAGTGCCAGAAC
 GGGGCCAGTGCATCGTGGTGCAGCAGGAGCCACCTGCCGCTGCCACCAGGCTTCGCCGG
 CCCCAGATGCGAGAAGCTCATCACTGTCAACTTCGTGGGCAAAGACTCCTACGTGGAAC
 CCTCCGCCAAGGTCCGACCCCAGGCCAACATCTCCCTGCAGGTGGCCACTGACAAGGACA
 GGCATCCTCTACAAAGGAGACAATGACCCCCCTGGCACTGGAGCTGTACCAAGGGCAC
 GCAGCTGGTCTATGACAGCCTGAGTTCCCAACCACAGTGTACAGTGTGGAGACAGTG
 ATGATGGGCAGTTTCACAGTGTGGAGCTGGTGACGCTAAACCAGACCCCTGAACCTAG
 GACAAAGGAACCTCCAAAGAGCCTGGGAAGCTCCAGAAGCAGCCAGCAGTGGCAT
 CCCCCTCTACCTGGAGGCATCCCCACCTCCACCAGGCCTCTCCGCCTGCAGGCCAGGG
 ACCGGCCTCTAGGCGGCTCCACGGATGCATCCATGAGGTGCGCATCAACAAG
 GACTTCAAGGCCCTCCCACACAGTCCCTGGGGTGTCAACCAGGCTGCAAGTCTGCAC
 GTGCAAGCACGGCCTGTGCCGCTCCGTGGAGAAGGACAGCGTGGTGTGCGAGTGC
 GCTGGACCGGCCACTCTGCACCAAGGGGAGCCCTACTGCCTGTGCCAGGCCGG
 CATGGAAAATGTGTGGCAACTGGACCTCATACATGTGCAAGTGTGCCAGGGCTATGG
 GGACTTGTGTACAACAAGAAATGACTCTGCCAATGCCATGCTCAGCCTCAAGTGT
 GGCAGTGCCACATCTCAGACCAAGGGGAGCCCTACTGCCTGTGCCAGGCCGG
 GAGCACTGCCAACAAAGAGAATCCGTGCCTGGACAAGTAGTCCGAGAGGTG
 GAAAGGTTATGCATCATGTGCCACAGCCTCCAAGGTGCCATCATGGAATGT
 GTGGGCCCTGCTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGC
 GACGGCTCCTCGTTGTAGAAGAGGTGGAGAGACACTTAGAGTGCGGCTGC
 CTAAGCCCCCTGCCCTGCCACCTCTGGACTCCAGCTTGATGGAGTTGG
 ATGTGGGACCCCTGGTATTGACATGAAGGAAATGAAGCTGGAGAGGAAG
 AGAGAATATTAAGTATATTGAAAATAACAAAAAATAGAACT
 AAAAAAAAAAAAAAAA
 AAAAAA

FIGURE 112

MAPGWAGVGA AVRARLALALALASVLSGP PAVACPTKCTCSAASVDCHGLGLRAVPRGIPRN
 AERLDLDRNNITRITKMDFAGLK NL RVLHLEDNQSVIERGAFQDLKQLERLRLNKNLQVL
 PELLFQSTPKLTRLDS ENQIQGIPRKAFRGITDVKNLQLDNNHIS CIEDGAFRALRDLEIL
 TLNNNNISRILVTSFNHMPKIRTLRLHSNHLYCDCHLAWLSDWLQRRTVGQFTLCMAPVHL
 RGFNVADVQKKEYVCPAPHSEPPSCNANSISCPSPCTCSNNIVDCRGKGLMEIPANLPEGIV
 EIRLEQNSIKAI PAGAFTQYKKLK RID ISKNQISDIAPDAFQGLKSITS LVL VGNKITEIAK
 GLFDGLVSLQLLL NANKINCLRVNT FQDLQNLNLLS LYDNKLQTI SKGLFAPLQSI QTLHL
 AQNPVFVCDCHLKW LADYLQDNPIETSGARCSSPRRLANKRISQIKSKKFRCSGSEDYRSRFS
 SEC FMDLVCPEKCRCEGTIVDCSNQKLVRIPSHLPEYVTDLRLNDNEVS VLEATGIFKKLPN
 LRKINLSNNKIKEVREGAFDGAASVQELMLTGQNQLETVHGRVFRGLSGLKTLMRLRSNLISCV
 SNDTFA GLSSVRLLS LYDNRITTITPGAF TTLVSLSTINLLSNPFCNCNCHLAWLGKWL RKR
 IVSGNPRCQKPF FLKEIPIQDVAIQDFTCDGNEESSCQLSPRCPEQCTCMETVVRC SNKGLR
 ALPRGMPKDVT ELYLEG NHLTAVPRELSALRH LTIDLSNN SISMLTNYTF SNMSHLSTLIL
 SYNRLRCIPVHAFNGLRSLRVLT LH GNDI SSVP EG SFNDL TSLS HLA LGTNPLHCDCSLRWL
 SEWVKAGYKEPGI ARCSSPEPMADRLLLTT PTHRFQCKGPVDINIVAKCNACLSSPCKNNGT
 CTQDPVELYRCACPYSYKGKDCTVPINTCIQNPCQHGGTCHLSDSHKDGFSCSCPLGFEGQR
 CEINPDDCEDND CENNATCVDGINNYVCICPPNYTGE LCDEVIDHCVPELNLCQHEAKCIPL
 DKGFSC EC VPGYSGKLCETDN DDCVAHKCRHGAQC VDTINGYTCTCPQGFSGP FCEH PPPMV
 LLQTSPCDQYE CQNGAQCIVVQQEPTCRCPPGFAGPRCEKLITVN FVGKDSY VELASAKVRP
 QANISLQVATDKDNGILL YKGDNDPLALELYQGHVRLVYDSLSSPPTVYS VETVNDGQFHS
 VELVTLNQTLN L VVDKGTPKSLGKLQKQPAVGINSPLYLG GIPTSTGLS ALRQGTDRPLGGF
 HGC IHEVRIN NELQDFKALPPQSLGVSPGCKSCTVCKHGLCRSVEKDSVCECRPGWTGPLC
 DQEARDPCLGHRCHHGKCVATGT SYMCKCAEGYGGDLCDNKNDSANACS AFKCHHGQCHISD
 QGEPYCLCQPGFSGEH CQQENPCLGQVVRE VIRRQKGYASCATASKV PIMECRRGGCGPQCCQ
 PTRSKRRKYVFQCTDGSSFVEEVERHLECGCLACS

Signal peptide:

amino acids 1-27

FIGURE 113

GGATGCAGGACGCTCCCTGAGCTGCCTGTCACCGACTAGGTGGAGCAGTGTTCCTCCGCA
GAECTCAACTGAGAAGTCAGCCTCTGGGGCAGGCACCAGGAATCTGCCTTTCAGTTCTGTCT
CCGGCAGGCTTGAGGATGAAAGGCTGCCATTCTGACCCCTATTGGCTGCCCTGGTCACAG
GCGCCGAGTCCAAAATCTACACTCGTTGCAAACGGCAAAATATTCTCGAGGGCTGCCCTG
GACAATTACTGGGCTTCAGCCTGGAAACTGGATCTGCATGGCATATTATGAGAGCGGCTA
CAACACCACAGCCCCGACGGTCCTGGATGACGGCAGCAGTCACTATGGCATCTCCAGATCA
ACAGCTTCGCGTGGTGCAGACGCGGAAAGCTGAAGGAGAACAAACCAACTGCCATGTCGCCTGC
TCAGCCTTGATCACTGATGACCTCACAGATGCAATTATCTGTGCCAGGAAAATTGTTAAAGA
GACACAAGGAATGAACTATTGCAAGGCTGGAAGAACATTGTGAGGGCAGAGACCTGTCCG
1 AGTGGAAAAAAGGCTGTGAGGTTCCTAAACTGGAACTGGACCCAGGATGCTTGCAGCAAC
GCCCTAGGATTGCACTGAAATGTCCAAATGCCTGTGTATCTTGTCCCCTTCCAAATA
TTCCTTCTCAAACCTGGAGAGGGAAAATTAAGCTATACTTTAAGAAAATAATTTCCAT
TTAAATGTC

FIGURE 114

MKAAGILTIGCLVTGAESKIKYTRCKLAKIFSRAGLDNWGFSLGNWICMAYYESGYNTTAP
TVLDDGSIDYGIFQINSFAWCRRGKLKENNHCHVACSLITDDLTDATIICARKIVKETQGMN
YWQGWKKHCEGRDLSEWKKGCEVS

Signal peptide:

amino acids 1-19

1 10 20 30 40 50 60 70 80 90 100

FIGURE 115

CAGGCCATTGCATCCCACTGTCCTGTGGAGCCAGGCCACACCGTCCTCAGCAGTGT
 CATGTGTTAAAAACGCCAAGCTGAATATATC**ATG**CCCCTATTAAAACCTGTACATGGCTCCC
 CATTGGTTTGAGAAAAGTTCAAGCTTTACCTTGGTGTGCCTGTATCCCAGTGTTC
 AGGCTGGCTAGACGGCGGAAGAACGATCCTATTTACTGTCACTTCCCAGATCTGCTTCAC
 CAAGAGAGATTCTTCTAAACGACTATACAGGGCCCCAATTGACTGGATAGAGGAATACA
 CCACAGGCATGGCAGACTGCATCTAGTCAACAGCCAGTTCACAGCTGCTGTTTAAGGAA
 ACATTCAAGTCCCTGTCTCACATAGACCCGTATGTCCTCTATCCATCTCTAAATGTACCAG
 CTGGTACTCAGTTGTTCTGAAAAGCTGGATGACCTAGTCCCCAAGGGGAAAAAATTCTGC
 TGCTCTCCATCAACAGATACGAAAGGAAGAAAAATCTGACTTTGGCACTGGAAGCCCTAGTA
 CAGCTCGGTGGAAGATTGACATCCAAGATTGGGAGAGGGTTCATCTGATCGTGGCAGGTGG
 TTATGACGAGAGAGTCCTGGAGAATGTGGAACATTATCAGGAATTGAAGAAAATGGTCCAAC
 AGTCCGACCTTGGCCAGTATGTGACCTTCTGAGGTCTTCTCAGACAAACAGAAAATCTCC
 CTCCTCCACAGCTGCACGTGTGCTTACACACCAAGCAATGAGCATTGGCATTGTCCC
 TCTGGAAGCCATGTACATGCAGTCCCCAGTCATTGCTGTTAATTGGGTGGACCCTTGGAGT
 CCATTGACCACAGTGTACAGGGTTCTGTGTGAGCCTGACCCGGTGCACTTCTCAGAAC
 ATAGAAAAGTTCATCCGTGAAACCTCCTAAAAGCCACCATGGGCTGGCTGGAAGAGCCAG
 AGTGAAGGAAAAAATTTCCTGAAAGCATTTACAGAACAGCTCTACCGATATGTTACCAAAC
 TGCTGGTA**TAA**TCAAGATTGTTTAAGATCTCCATTAAATGTCATTGTTATGGATTGTAGACC
 CAGTTTGAAACCAAAAAAGAACCTAGAATCTAATGCAGAAGAGATCTTTAAAAAATAAA
 CTTGAGTCTGAATGTGAGCCACTTCCTATATACCAACACCTCCGTCCACTTTCAGAAA
 AACCATGTCTTATGCTATAATCATTCAAATTGGCCAGTGTAAAGTTACAAATGTGGTG
 TCATTCCATGTCAGCAGAGTATTAAATTATATTCTCGGGATTATTGCTCTGTCTA
 TAAATTGAAATGATACTGTGCCTTAATTGGTTTCAAGTTAAGTGTGTATCATTCAA
 AGTTGATTAATTGGCTTCAGTATAATGAGAGCAGGGCTATTGTAGTCCAGATTCAAT
 CCACCGAAGTGGTCACTGTCATCTGTTAGGAAATTGGTGTCTGTCTTGCCTGGATC
 CATAGCGAGAGTGCTCTGTATTGTTAAGATAATTGTATTGCAACTGAGATATAA
 TAAAAGGTGTTATCATAAAAAAAAAAAAAAA

FIGURE 116

MPLLKLVHGSPLVFGEFKLFTLVSACIPVFRLARRKKILFYCHFPDLLTKRDSFLKRLY
RAPIDWIEEYTTGMADCILVNSQFTAASFVKETFKSLSHIDPDVLYPSLNVTSDSVVPEKLD
DLVPKGKKFLLSINRYERKKNLTLALEALVQLRGRLTSQDWERVHLIVAGGYDERVLENVE
HYQELKKMVQQSDLGQYVTFLRSFSDKQKISLLHSCTCVLYTPSNEHFGIVPLEAMYMQCPV
IAVNSGGPLESIDHSVTGFLCEPDPVHFSEAIKEFIREPSLKATMGLAGRARVKEKFSPPEAF
TEQLYRYVTKLLV

Signal peptide:

amino acids 1-15

FIGURE 117

GACTACGCCGATCCGAGACGTGGCTCCCTGGCGGCAGAACCAATGTGGACTTCGCGATCTT
 CGCCGTTACCTTCTTGCTGGCGTGGTGGGAGCCGTGCTCACCTCTATCCGGCTTCCAGAC
 AAGCTGCAGGAATTCCAGGGATTACTCCAACCTGAAGAAAAAGATGGTAATCTTCCAGATATT
 GTGAATAGTGGAAAGTTGCATGAGTTCTGGTTAATTGCATGAGAGATATGGCCTGTGGT
 CTCCTCTGGTTGGCAGGCGCCTCGTGGTAGTTGGCACTGTTGATGTACTGAAGCAGC
 ATATCAATCCAATAAGACATCGGACCCTTGAAACCAGTGAAGTCATTATTAAGGTAT
 CAATCTGGTGGTGGCAGTGTGAGTGAAAACCACATGAGGAAAAATTGTATGAAAATGGTGT
 GACTGATTCTCTGAAGAGTAACTTGCCCTCCTAAAGCTTCAGAAGAATTATTAGATA
 AATGGCTCTCCTACCCAGAGACCCAGCACGTGCCCTCAGCCAGCATATGCTTGGTTTGCT
 ATGAAGTCTGTTACACAGATGGTAATGGTAGTACATTGAAGATGATCAGGAAGTCATTG
 CTTCCAGAAGAACATGGCACAGTTGGTCTGAGATTGGAAAAGGCTTCAGATGGTCAC
 TTGATAAAAACATGACTCGGAAAAAACAAATATGAAGATGCCCTCATGCAACTGGAGTCTGTT
 TTAAGGAACATCATAAAAGAACGAAAAGGAAGGAACCTCAGTCAACATATTTCATTGACTC
 CTTAGTACAAGGGAACCTTAATGACCAACAGATCCTAGAAGACAGTATGATATTTCTCTGG
 CCAGTTGCATAATAACTGCAAAATTGTGTACCTGGCAATCTGTTTTAACCACCTCTGAA
 GAAGTTCAAAAAAAATTATATGAAGAGATAAACCAAGTTGGAAATGGCCTGTTACTCC
 AGAGAAAATTGAGCAGCTCAGATATTGTCAGCATGTGCTTGTGAAACTGTTGAACTGCCA
 AACTGACTCCAGTTCTGCCAGCTCAAGATATTGAAGGAAAATTGACCGATTTATTATT
 CCTAGAGAGACCCCTGTCCTTATGCCCTGGTGTGGTACTTCAGGATCCTAATACTGGCC
 ATCTCCACACAAGTTGATCCAGATCGGTTGATGAATTAGTAATGAAAACCTTTCT
 CACTTGGATTCTCAGGCACACAGGAGTGTCCAGAGTTGAGGTTGCATATATGGTACCAC
 GTACTTCTTAGTGTATTGGTGAAGAGACTGCACCTACTTCGTGGAGGGACAGGTTATTGA
 AACAAAGTATGAACTGGTAACATCATCAAGGGAAGAAGCTGGATCACTGTCTCAAAGAGAT
 ATTTAAATTTATACATTAAAATCATTGTTAAATTGATTGAGGAAAACAACCATTAAAAAA
 AAATCTATGTTGAATCCTTATAAACCAAGTATCAGTTGTAATATAAACACCTATTTGTAC
 TTAA

FIGURE 118

MLDFAIFAVTFLLALVGAVLYLYPASRQAAGIPGIPTEEKDGNDLPIVNSGSLHEFLVNLH
ERYGPVVSFWFGRRLVVSLGTVDVLKQHINPNKTSDPFETMLKSLLRYQSGGGSVSENHMRK
KLYENGVTDSLKSNFALLKLSEELLDKWLSYPETQHVPLSQHMLGFAMKSVTQMVMGSTFE
DDQEVEIRFQKNHGTVWSEIGKGFLDGSLDKNMTRKKQYEDALMQLESVLRNIIKERKGRNFS
QHIFIDSLVQGNLNDQQILEDMSIFSLASCIITAKLCTWAICFLTSEEVQKKLYEEINQVF
GNGPVTPEKIEQLRYCQHVL CETVRTAKLTPVSAQLQDIEGKIDRFIIPRETLVLYALGVVL
QDPNTWPSPHKFDPDRFDELVMKTFSSLGFSGTQECPELRFAYMVTIVLLSVLVKRLHLLS
VEGQVIETKYELVTSSREEAWITVSKRY

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 271-290

FIGURE 119

CTAGATTGTCGGCTTGC~~GGGG~~GACTTCAGGAGTCGCTGTCTGAAC~~TCCAGCCTCAGA~~
GACCGCCGCC~~TTGT~~CCCCGAGGCC**ATG**GGCCGGGCTCAGGGCTTG~~GCC~~CTCGCTTC
CTGACGCTCCTGGCGCATCTGGTGGTCGT~~CATCAC~~CTTATTCTGGTCCC~~GGG~~A~~CAGCAAC~~AT
ACAGGCCTGCCTGCCTC~~ACG~~TT~~ACCCCCGAGGAGTATGACAAGCAGGACATT~~CAGCTGG
TGGCCGCGCTCTGT~~CAC~~CTGGCCT~~TTG~~CAGTGGAGCTGGCCGGTT~~CC~~CTCAGGA
GTCTCCATGTTAACAGCACCCAGAGCCT~~CATCT~~CCATTGGGCTCA~~TGTAGTGCATCCGT~~
GGCC~~CTGT~~C~~TTCTT~~CATATT~~CGAGCGTTGGAGTGC~~ACTACGTATTGGTACATTTGTCT
TCTGCAGTGCC~~CTT~~CCAGCTGT~~C~~ACTGAAATGG~~CTT~~ATT~~CGT~~ACC~~GT~~CTTGGGCTGAAA
AAGAAACCC~~TTCTGA~~TTAC~~CTTC~~CATGAC~~GGGAAC~~CTAAGGACGAAGCCTACAGGGGCAAGGG
CCGCTTCGTATT~~CC~~TGGAA~~AGAAGGAAGG~~CATAGGCTT~~CGG~~TTT~~CC~~CTCG~~AA~~ACTGCTTC
TGCTGGAGGATATGTGTT~~GGAAATAATTAC~~GT~~CTTGAGTCTGGGATTATCCG~~CATTGTATT~~TA~~
GTGCTT~~GTAATAAAATATGTTGTAGTAACATTAAGACTTATACAG~~TTAGGGGACA
ATTAAAAAAA

FIGURE 120

MGRVSGLVPSRFLTLLAHLVVVITLFWSRDSNIQACLPLTFTPEEYDKQDIQLVAALSVTLG
LFAVELAGFLSGVSMFNSTQSLISIGAHCSASVALSFFIFERWECTTYWYIFVFCSALPAVT
EMALFVTVFGLKKKPF

Transmembrane domain:

amino acids 12-28 (type II), 51-66, 107-124

FIGURE 121

TCCC GGAC CCTGCCGCCCTGCCACT **ATGT** CCCGCCGCTCTATGCTGCTTGCCTGGGCTCTCC
 CCAGC CCTC TTGACTCGGAGCGGCTCAGGAGACAGAAGACCCGGCCTGCTGCAGCCCCATA
 GTGCCCGGAACGAGTGGAAAGGCCCTGGCATCAGAGTGC GCCCAGCACCTGAGCCTGCCCTT
 ACGCTATGTGGTGGTATCGCACACGGCGGGCAGCAGCTGCAACACCCCCGCCTCGTGCCAGC
 AGCAGGCCCGGAATGTGCAGCACTACCACATGAAGACACTGGGCTGGTGCACGTGGCTAC
 AACTCCTGATTGGAGAAGACGGGCTCGTATACGAGGGCCGTGGCTGGAACTTCACGGGTGC
 CCACTCAGGTCACTTATGGAACCCATGTCCATTGGCATCAGCTTCATGGCAACTACATGG
 ATCGGGTGCCACACCCAGGCCATCCGGCAGCCCAGGGTCTACTGGCCTGC GGTGTGGCT
 CAGGGAGCCCTGAGGTCCA ACTATGTGCTCAAAGGACACC GGGATGTGCAGCGTACACTCTC
 TCCAGGCAACCAGCTCTACCACCTCATCCAGAATTGGCCACACTACCGCTCCCC **TGAGGCC**
 CTGCTGATCCGCACCCATTCCCTCCCTCCATGCCAAAAACCCC ACTGTCTCCTTCTCCA
 ATAAAGATGTAGCTC

FIGURE 122

MSRRSMLLAWALPSLLRLGAAQETEDPACCSPIVPRNEWKALASECAQHLSLPLRYVVVSHT
AGSSCNTPASCQQQARNVQHYHMKTILGWCDVGYNFLIGEDGLVYERGRWNFTGAHSGHLWNP
MSIGISFMGNYMDRVPTPQAIRAAQGLLACGVAQGALRSNYVLKGHRDVQRTLSPGNQLYHL
IQNWPHYRSP

Signal peptide:

amino acids 1-20

100 90 80 70 60 50 40 30 20 10 0 %

FIGURE 123

CTGGGACCCCGAAAAGAGAAGGGGAGAGCGAGGGGACGAGAGCGGAGGAAG**ATG**CAACT
 GACTCGCTGCTGTTCTGGTGCAGGGTAGCCTCTATCTGGTCATCTGTGGCCAGG
 ATGATGGTCCTCCGGCTCAGAGGACCTGAGCGTGATGACCACGAGGGCAGCCCCGGCCC
 CGGGTGCCTCGGAAGCGGGGCCACATCTCACCTAACGAGTCCCAGGGCATGGCAATTCCACTCT
 CCTAGGGCTGCTGGCCCCGCCTGGGGAGGCTTGGGCATTCTTGGCAGCCCCCAACCGCC
 CGAACACAGCCCCCACCCCTCAGCCAAGGTGAAGAAAATCTTGGCTGGGCAGTCTAC
 TCCAACATCAAGACGGTGGCCCTGAACCTGCTCGTCACAGGAAAGATTGTGGACCATGGCAA
 TGGGACCTTCAGCGTCCACTTCAAACACAATGCCACAGGCCAGGGAAACATCTCCATCAGCC
 TCGTCCCCCAGTAAAGCTGTAGAGTTCCACCAGGAACAGCAGATCTTCATCGAAGCCAAG
 GCCTCCAAAATCTCAACTGCCGGATGGAGTGGGAGAAGGTAGAACGGGCCGGACCTC
 GCTTGACCCACGCCAGCAAGATCTGCTCCGAGACCACGCTCAGAGCTCAGCCACCT
 GGAGCTGCTCCAGCCCTCAAAGTCGTCTGTCTACATGCCCTTACAGCACGGACTAT
 CGGCTGGTCCAGAAGGTGTGCCAGATTACAACCTACCATAGTGTACCCCCCTACTACCCATC
 TGGG**TGA**CCCAGGGCAGGCCACAGAGGCCAGGGCTGGAAGGACAGGCCCTGCCATGC
 AGGAGACCATCTGGACACCAGGGCAGGGAAAGGGTTGGGCCTCAGGCAGGGAGGGGGTGGAG
 ACGAGGAGATGCCAAGTGGGCCAGGGCCAAGTCTCAAGTGGCAGAGAAAGGGTCCAAGTG
 CTGGTCCAAACCTGAAGCTGTGGAGTGACTAGATCACAGGAGCACTGGAGGAGGTGGCT
 CTCTGTGCAGCCTCACAGGGCTTGCCACGGAGCCACAGAGAGATGCTGGGTCCCCGAGGCC
 TGTGGCAGGCCGATCAGTGTGGCCCCAGATCAAGTCATGGAGGAAGCTAACCCCTGGTT
 CTTGCCATCCTGAGGAAAGATAGCAACAGGGAGGGGAGATTCATCAGTGTGGACAGCCTG
 TCAACTTAGGATGGATGGCTGAGAGGGCTTCCCTAGGAGCCAGTCAGCAGGGTGGGTGGGC
 CAGAGGAGCTCTCAGCCCTGCCTAGTGGCGCCCTGAGCCCTTGTGCTGCTGAGCATG
 GCATGAGGCTGAAGTGGCAACCCCTGGGTCTTGATGTCTTGACAGATTGACCATCTGTCTC
 CAGCCAGGCCACCCCTTCCAAAATCCCTCTTCAAGCTAACAGACAGGACGATTGTGGCTCCACACTAACGGCC
 ACAGCCCATCCGCGTGTGTCCTTCCACCCCAACCCCTGCTGGCTCCTCTGGGAG
 CATCCATGTCCCGAGAGGGGTCCTCAACAGTCAGCCTCACCTGTGAGACCCGGGTTCTCC
 CGGATCTGGATGGCGCCGCCCTCTCAGCAGGGCACGGGTGGGCGGGCCGGCCGCAGA
 GCATGTGCTGGATCTGTTCTGTGTCTGTGTTGGGTGGGGAGGGAGGGAAAGTCTGT
 GAAACCGCTGATTGCTGACTTTGTGTGAAGAACGTGTTCTGGAGCAGGAATAAGCTT
 GCCCCGGGGCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66521
><subunit 1 of 1, 252 aa, 1 stop
><MW: 28127, pI: 8.91, NX(S/T): 5
MQLTRCCFVFLVQGSLYLVICGQDDGPPGSEDPERDDHEGQPRPRVPRKRGHISPKSRPMAN
STLLGLLAPPGEAWGILGQPPNRPNHSPPPSAKVKKIFGWGDFYSNIKTVANLLVTGKIVD
HGNNTFSVHFQHNATGQGNISISLVPPSKAVEFHQEQQIFIPEAKASKIFNCRMEWEKVERGR
RTSLCTHDPAKICSRDHAQSSATWSCSQPKVVCVYIAFYSTDYRLVQKVCPDNYHSDTPY
YPSG
```

Important features of the protein:

Signal peptide:

amino acids 1-14

N-glycosylation sites.

amino acids 62-65, 127-130, 137-140, 143-146

2-oxo acid dehydrogenases acyltransferase

amino acids 61-71

FIGURE 125

GTGAATGTGAGGGTTGATGACTTCAGATGTCTAGGAACCAGAGTGGTGCAGGGGCCCA
 GGCAGGGCTGATTCTGGCGGGAGAGTAGGGTAAAGGGTCTGCATGAGCTCCTAAAG
 GACAAAGGTAACAGAGCCAGCGAGAGAGCTCGAGGGAGACTTGACTTCAAGCCACAGAAT
 TGGTGGAAAGTGTGCGCGCCGCCGCGCTCGCTCCTGCAGCGCTGTCGACCTAGCCGCTAG
 CATCTTCCCAGCACCAGGATCCCGGGTAGGAGGGACGCAGGGGAGCACAGGCCAGCC
 GGCTGCGGCTGCCACACGGCTACCA**AT**GGGCTCCGGCGCCGGCTGTCGCGGTGCCG
 GCCGTGCTGCTGGTCTCACGCTGCCGGGCTGCCGTCTGGGACAGAACGACACGGAGCC
 CATCGTGTGGAGGGCAAGTGTCTGGTGGTGTGCGACTCGAACCCGGCACGGACTCCAAGG
 GCTCCTCTTCCCTCCCCGCTGGGATATCGGTCCGGCGGCCACTCCAAGGTGCGCTTCTCG
 GCAGGGTGCAGGACCAACCACGAGCCATCCGAGATGAGCAACAAGACGCGCATCATTACTT
 CGATCAGATCCTGGTGAATGTGGTAATTTTCACATTGGAGTCTGTCTTGTAGCACCAA
 GAAAAGGAATTACAGTTCAGTTCACGTGATTAAAGTCTACCAGAGCCAAACTATCCAG
 GTTAACTTGATGTTAAATGGAAAACCAGTAATATCTGCCTTGCGGGGACAAAGATGTTAC
 TCGTGAAGCTGCCACGAATGGTGCCTGCTCACCTAGATAAAGAGGATAAGGTTACCTAA
 AACTGGAGAAAGGTAAATTGGTGGAGGCTGGCAGTATTCCACGTTCTGGCTTCTGGT
 TTCCCCCTA**TAG**GATTCAATTCTCCATGATGTTCATCCAGGTGAGGGATGACCCACTCCTG
 AGTTATTGGAAGATCATTTCATCATTGGATTGATGTCTTTATTGGTTCTCATGGTG
 GATATGGATTCTAAGGATTCTAGCCTGTCGAACCAATAACAAATTTCACAGATTATTGTG
 TGTGTCTGTTCACTATTTGGATTGGACTCTAACAGATAAACCTATGCTTAAATGTA
 ACAGTCAAAAGCTGTGCAAGACTTATTCTGAATTTCATTCTGGATTACTGAATTAGT
 TACAGATGTGGAATTTCATTGTTAGTTAAAGACTGGCAACCAGGTCTAAGGATTAGA
 AAACTCTAAAGTCTGACTCAATCACGGTTAGTGTGATACTGCCAAAGAACTGTATACTG
 TGTTAATATATTGATTATTTGTTTATTCTGGATTAGTTCTCTAAATAAGGTAATGAA
 AAAACTGGATTTTTCTAGTAACGGTATTATGTTCTCTAAATAAGGTAATGAA
 TGGCTGCCACAAATTACCTGACTACGATATCATGACATGACTCTCTAAAAAA
 GAATGCTTCATAGTTGATTTAATTGTATATGTGAAAGAGTCATATTCCAAGTTATATT
 TTCTAAGAAGAAGAATAGATCATAAATCTGACAAGGAAAAGTTGCTTACCCAAATCTAAG
 TGCTCAATCCCTGAGCCTCAGCAAAACAGCTCCCGAGGGAAACTTCTACTTATTGC
 TCAACTTAATTAAATGATTGATAATAACCACCTTATTAAAAACCTAACGGTTTTTT
 TCCGTAGACATGACCACTTATTAAACTGGTGGTGGGATGCTGTTCTAATTACCTAT
 TTTCAAGGCTCTGTTGATTTGAAGTATCATCTGGTTTGCCTTAACCTTAAATTGTA
 TATATTATCTGTTAGCTAATATTAAATTCAAATATCCCATATCTAAATTAGTGAATAT
 CTTGCTTTGTATAGGTCAATTCAAAATTATTATGTCTGTTATAGAATAAAGA
 TTAATATATGTTAAAAAA

FIGURE 126

MGSRRALSAVPAVLLVLTPGLPVWAQNDTEPIVLEGKCLVVCDNSNPATDSKGSSSPLGI
SVRAANSKVAFAFSAVRSTNHEPSEMSNKTRIIYFDQILVNVGNNFTLESVFVAPRKGIYSFSF
HVIKVYQSQTIQVNLMNLNGKPVISAFAGDKDVTREAATNGVLLYLDKEDKVYILKLEKGNLVG
GWQYSTFSGFLVFPL

Signal peptide:

amino acids 1-27

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27

FIGURE 127

CGGTGGCC**ATG**ACTGCGGCCGTGTTCTCGGCTGCGCCTCATTGCCTTCGGCCTGCGCTC
 GCCCTTATGTCTCACCATGCCATCGAGCCGTTGCGTATCATCTTCCTCATGCCGGAGC
 TTTCTCTGGTTGGTGTCTACTGATTCGTCCCTGTTGGTTCATGGCAAGAGTCATTA
 TTGACAACAAAGATGGACCAACACAGAAATATCTGCTGATCTTGAGCGTTGTCTGTC
 TATATCCAAGAAATGTTCCGATTGCATATTATAAACTCTTAAAAAAAGCCAGTGAAGGTTT
 GAAGAGTATAAACCCAGGTGAGACAGCACCCCTATGCGACTGCTGGCCTATGTTCTGGCT
 TGGGCTTGGAAATCATGAGTGGAGTATTCCTTGTGAATACCCTATCTGACTCCTGGGG
 CCAGGCACAGTGGCATTCATGGAGATTCTCCTCAATTCTCCTTATTGACCTTCATGAC
 GCTGGTCATTATCTGCTGCATGTATTCTGGGCATTGTATTTTGATGGCTGTGAGAAGA
 AAAAGTGGGGCATCCTCCTTATCGTTCTCCTGACCCACCTGCTGGTGTAGCCCAGACCTTC
 ATAAGTTCTTATTATGGAATAAACCTGGCGTCAGCATTATAATCCTGGTGTATGGCAC
 CTGGGCATTCTTAGCTGCGGGAGGCAGCTGCCGAAGCCTGAAACTCTGCCTGCTGCCAAG
 ACAAGAACTTCTTACAACCAGCGCTCCAGA**TAA**CCTCAGGAAACCAGCACTCCCAA
 ACCGCAGACTACATCTTAGAGGAAGCACAACGTGCCTTTCTGAAAATCCCTTTCTG
 GTGGAATTGAGAAAGAAATAAAACTATGCAGATA

1000
 1500
 2000
 2500
 3000
 3500
 4000
 4500
 5000

FIGURE 128

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66658
><subunit 1 of 1, 257 aa, 1 stop
><MW: 28472, pI: 9.33, NX(S/T): 0
MTAAVFFGCAFIAGPALALYVFTIAIEPLRIIFLIAGAFFWLVSLLISSLVWFMARVIIDN
KDGPTQKYLLIFGAFVSVYIQEMFRFAYYKLLKKASEGLKSINPGETAPSMRLLAYVSGLGF
GIMSGVFSFVNTLSDSLGP GTVGIHGDSPQFFLYSAFMTLVIIILLHVFWGIVFFDGCEKKW
GILLIVLLTHLLVSAQTFI SYYGINLASAFIILVLMGTWAFLAAGGSCRSLKLCLLCQDKN
FLLYNQRSR
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domains:

amino acids 32-51, 119-138, 152-169, 216-235

Glycosaminoglycan attachment site.

amino acids 120-123

Sodium:neurotransmitter symporter family protein

amino acids 31-65

FIGURE 129

CGGCAACCAGCCGCCACCACCGCTGCCACTGCCGCCCTGCCGGGGC**A**TGTTCGCTCTGGGCTTGCCTTCT
 TGGTGCCTTGGTGGCCTCGGTGAGAGCCATCTGGGGTTCTGGGGCCAAGAACGTCTCGAGAAAGACGCCG
 AGTTTGAGCGCACCTACGTGGACGAGGTCAACAGCGAGCTGGTCAACATCTACACCTCAACCATACTGTGACCC
 GCAACAGGAACAGAGGGCGTGCCTGTCAGTGAACAGCAGAAGGGGGCGCCGTTGCTGTTGTGG
 TCCGCCAGAAGGAGGCTGTGGTGCCTCCAGGTGCCCTAATCCTGCAGGGATGTTCAGCGCAAGTACCTCT
 ACCAAAAAGTGGAACGAACCTGTGTCAGCCCCCACCAGAAGAATGAGTCGGAGATTAGTCTTCTACGTGGATG
 TGTCCACCCCTGTACCAGTCACACCATACCAAGCTCCGGTCAGCCGATGGACGATTTGTGCTCAGGACTG
 GGGAGCAGTTCAGCTCAATACCACAGCAGCACAGCCCCAGTACTTCAGTGAAGTATGAGTCCCTGAAGGCGTGGACT
 CGGTAAATTGTCAAGGTGACCTCAACAAGGCCCTCCCTGTCAGTCATCTCATTAGGATGTGCTGTCCTG
 TCTATGACCTGGACAACAACGTAGCCTTCATCGGCATGTACCAAGACGATGACCAAGAAGGCGGCATCACCGTAC
 AGCGCAAAGACTCCCCAGCAACAGCTTTATGTGGTGGTGGTGAAGACCGAAGACCAAGCCTGCGGGGCT
 CCCTGCCCTTCTACCCCTCGCAGAAGATGAACCGTCGATCAAGGGCACCAGAAAACCTGTCAGTGTGCTGG
 TGTCTCAAGCAGTCACGTCAGGCATACGTCACTGGGATGCTTTGCTGGTATATTCTCCTTCTTAC
 TGCTGACCGTCCTCTGGCCTGCTGGGAGAACTGGAGGAGAAGAAGAACCTGCTGGTGGCATTGACCGAG
 CCTGCCAGAAGCGGTACCCTCGAGTCTGGTGAATTCTTCTGGCAGTTCCCCTATGAGGGTTACAAC
 ATGGCTCTTGAGAATGTTCTGGATCTACCGATGGTCTGGTGAACAGCGCTGGCACTGGGACCTCTTACG
 GTTACCAAGGGCGCTCTTGAAACCTGTAGGTACTCGGCCCGAGTGGACTCCATGAGCTCTGTGGAGGAGATG
 ACTACGACACATTGACCGACATCGATTCCGACAAGAACATGTCATTGCAACAGCAATACCTCTATGTGGCTGACC
 TGGCACGGAAGGACAAGCGTGTCTCGCGAAAAAGTACCAAGATCTACTCTGGAACATTGCCACATTGCTGTCT
 TCTATGCCCTCTGTGGTCACTGGTGTACCTACCAAGACGGTGTGAATGTCACAGGGAAATCAGGACATCT
 GCTACTACAACCTCCTCTGCCACCCACTGGCAATCTCAGCGCCTCAACAACATCCTCAGCAACCTGGG
 ACATCCTGCTGGGGCTGCTTCTGTCATCATCTGCAACCGGAGATCAACCCACAACCGGGCCTGCTGCGCA
 ATGACCTCTGTGCCCCGATGGGAAATGTTGGGATCCCCAACACTTGGGCTTCTACGCCATGGGACAGCCCTGATGA
 TGGAGGGCTGCTCAGTCCTGCTATCATGTGCCCCAACTATAACCAATTCCAGTTGACACATCGTTCATGT
 ACATGATGCCGGACTCTGCATGCTGAAGCTCTACCAAGACGGGACCCGGACATCAACGCCAGGCCCTACAGT
 CCTACGCTGCTGCCATTGTCATCTCTCTGTGCTGGCTGGTCTTGCAAGGGAAACACGGCTTCT
 GGATCGCTCTCCATCATTACATCATGCCACCCCTGCTCCTCAGCACGCTCTATTACATGGGCGGTGGA
 AACTGGACTCGGGGATCTCCCGCGCATCTCCACGTGCTCTACACAGACTGCACTGGGCAAGTGCAGCGGGCG
 TCTACGTTGGACCGCATGGTGTGCTGGTCATGGCAACGTCACTGGTCGCTGGCTGCCTATGGGCTTATCA
 TGCGCCCCATGATTGCTTCTACTTGGGCAATTGGCATCTGCAACCTGCTCCTTACTTCGCTTCTACA
 TCATCATGAAGCTCCGGAGTGGGAGAGGATCAAGCTCATCCCCCTGCTCTGCATGTTGCACCTCCGTGGTCT
 GGGGCTTCGCGCTCTCTTCTCAGGGACTCAGCACCTGGCAGAAAACCCCTGCAAGACTGAGGGAGCACA
 ACCGGGACTGCATCCTCTCGACTTCTTGACGACCACGACATCTGGCACTCCCTCTCCATGCCATGTTG
 GGTCCCTCTGGTGTGACACTGGATGACGACCTGGATACTGTGCAAGGGACAAGATCTATGTCTTCT**A**
 AGGAGCTGGCCCTTCGCTTCAACCTCAAGGGCCCTGAGCTCTTGTGTCATAGACCGGTCACTCTGTCGTGCT
 GTGGGGATGAGTCCACGCCAGCAGCTGCCAGCACTGGATGGCAGCAGGACAGCCAGGTCTAGCTTAGGCTTGGCCT
 GGGACAGCCATGGGGTGGCATGGAACCTTGCAGCTGCCCTCTGCCAGGGCTGCTCCCTGGAAACCCCC
 AGATGTTGGCCAATTGCTGCTTCTCTCAGTGTGGGGCCTCCATGGGCCCTGCTCTTGGCTCTCCATT
 GTCCCTTGCAAGAGGAAGGATGGAAGGGACACCCCTCCCCATTCTCATGCCCTGCAATTGGCCCTCCTCCCC
 ACAATGCCCGCAGCTGGGACCTAAGGCCATTCTTCTCCCTACTCCCACCTCCAGGGCTAGTCTGGGCTGA
 ATCTCTGCTCTGATCAGGGCCCCAGTTCTTGGGCTGCTGCCATCAGCTGCCATTCAGTCAGCC
 AGGATGGATGGGGTATGAGATTGGGGTTGGCCAGCTGGTGCCTAGGGCTGGCTTCTTAGCAATGCGCTCAGCCAAATT
 TGAGAACCGCTTCTGATTCAAGAGGCTGAATTCAAGGGCTCACCTCTCATCCCACAGCTCCAGACTGATGCC
 AGCACCAAGGACTGGAGGGAGAAGCGCCTCACCCCTCCCTCTTCAAGGGCTTAGTCTGCAACCCCC
 AGCTGGTGGCCTTCAGTGCCTTGACACTGCCAAGAACATGTCAGGGGCAAAGGAGGGATGATAACAGACTCAG
 CCCGTTCTGCCCTCACAGCTGGGACCCCCAGTGCTACCTTAGAAAGGGGCTTCAGGAAGGGATGTGCTGTT
 CCCTCTACGTGCCAGTCAGCCTCGCTAGGACCCAGGGCTGGCTCTAAGTTCCGTCAGTCTCAGGCC
 AGTTCTGTGTTAGTCATGCACACACATACCTATGAAACCTGGAGTTACAAAGAATTGCCAGCTCTGGCAC
 CCTGGCCACCCCTGGCTTGGATCCCCCTCGTCCCACCTGGTCACCCAGATGCTGAGGATGGGGAGCTCAGG
 CGGGGCTCTGCTTGGGATGGGAATGTGTTTCTCCAAACTGTTTATAGCTCTGCTGAAGGGCTGG
 AGATGAGGTGGGTCTGGATCTTCTCAGAGCGTCTCCATGCTATGGTTGCATTCCGTTTATGAATGAATT
 TGCATTCAATAACCAACAGACTCAAAAAAAAAAAAAA

FIGURE 130

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66659
><subunit 1 of 1, 832 aa, 1 stop
><MW: 94454, pI: 6.94, NX(S/T): 12
MFALGLPFLVLLVASVESHLGVLGPKNVSQKDAEFERTYVDEVNSELVNIYTFNHTVTRNRT
EGVRVSVNLNKQKGAPLLFVVRQKEAVVSFQVPLILRGMFQRKYLYQKVERTLCQPPTKNE
SEIQFFYVDVSTLSPVNTTYQLRVSRMDDFVLRTGEQFSNNTAAQPQYFKYEFPEGVDSVI
VKVTSNKAFPCSVISIQDVLCPVYLDNNVAFIGMYQTMTKKAITVQRKDFPSNSFYVVVV
VKTEDQACGGSLPFYPFAEDEPVQDQGHROKTLSDLVSQAVTSEAYVSGMLFCLGIFLSFYLL
TVLLACWENWRQKKKTLVAIDRACPESGHPRVLADSFPGSSPYEGNYGSFENVSGSTDGL
VDSAGTGDLSYGYQGRSFEPVGTRPRVDSMSSVEEDDYDTLTDIDS DKNVIRTKQYLYVADL
ARKDKRVLRKKYQIYFWNIATIAVFYALPVVQLVITYQTVVNVTGNQDICYYNFLCAHPLGN
LSAFNNILSNLGYILLGLLFLLIIILQREINHNRA LLRN DLCALECGIPKHFGFLFYAMGTALM
MEGLLSACYHVCPTYNFQFDTSFMYMIAGLCMLKLYQKRHPDINASAYSAYACLAIVIFFS
VLGVVFGKGNTAFWIVFSIIHIIATLLLSTQLYYMGRWKLDGIFRRILHVLYTDCIRQCSG
PLYVDRMVLLVMGNVINWSLAAYGLIMRPNDFASYLLAIGICNLLYFAFYIIMKLRSGERI
KLIPLL CIVCTS VVWG FALFFFQGLSTWQKTPAESREHN RDCILL DFFDDHD IWHFLSSIA
MFGSFLVLLTLDDLD TVQR DKIYVF
```

Important features of the protein:**Signal peptide:**

amino acids 1-18

Transmembrane domains:

amino acids 292-317, 451-470, 501-520, 607-627, 751-770

Leucine zipper pattern.

amino acids 497-518

N-glycosylation sites.

amino acids 27-30, 54-57, 60-63, 123-126, 141-144, 165-168, 364-367, 476-479, 496-499, 572-575, 603-606, 699-702

FIGURE 131

GCTCAAGTGCCTGCCCTGCCCCACCCAGCCCAGCCTGGCCAGAGCCCCCTGGAGAAGGAGC
 TCTCTTCTTGCTTGGCAGCTGGACCAAGGGAGCCAGTCTTGGCTCTCCGTCCCCCAGGCTCTCCCAAGGC
 ACC**TG**TCCTGCCTGGCTGTGGCTGTTGTCTCCGTCCCCCAGGCTCTCCCAAGGC
 CCAGCCTGCAGAGCTGTCTGTGGAAGTTCAGAAAATATGGTGGAAATTCCCTTATACC
 TGACCAAGTTGCCGCTGCCCGTGAAGGGGCTGAAGGCCAGATCGTGTGTCAGGGACTCA
 GGCAAGGCAACTGAGGGCCATTGCTATGGATCCAGATTCTGGCTTCTGCTGGTACCCAG
 GGCCTGGACCGAGAGGAGCAGGAGTACAGCTACAGGTACCCCTGGAGATGCAGGATG
 GACATGTCTTGTGGGGTCCACAGCCTGTGCTGTGACGTGAAGGATGAGAATGACCAGGTG
 CCCCATTCTCTCAAGCCATCTACAGAGCTGGCTGAGCCGGGTACCAAGGCCTGGCATCCC
 CTTCCTCTCCTTGAGGCTTCAGACGGGATGAGCCAGGCACAGCCAACTCGGATCTCGAT
 TCCACATCCTGAGCCAGGCTCCAGCCCAGCCTCCCCAGACATGTTCCAGCTGGAGCCTCGG
 CTGGGGCTCTGGCCCTCAGCCCCAAGGGGAGCACAGCCTGACCACGCCCTGGAGAGGAC
 CTACCAAGCTGTTGGTACAGGTCAAGGACATGGGTGACCAGGCCCTCAGGCCACCAAGGCCACTG
 CCACCGTGGAAAGTCTCCATCATAGAGAGCACCTGGGTGTCCTAGAGCCTATCCACCTGGCA
 GAGAATCTCAAAGTCTTACACCCGACCATGGCCCAGGTACACTGGAGTGGGGTGTATGT
 GCACTATCACCTGGAGAGCCATCCCCGGGACCTTGAAGTGAATGCAGAGGGAAACCTCT
 ACGTGACCAGAGAGCTGGACAGAGAACGCCAGGCTGAGTACCTGCTCCAGGTGCGGGCTCAG
 AATTCCCATGGGAGGACTATGCGGCCCCCTCTGGAGCTGCACGTGCTGGTGTGGATGAGAA
 TGACAACGTGCCTATCTGCCCTCCCCGTGACCCACAGTCAGCATCCCTGAGCTCAGTCCAC
 CAGGTACTGAAGTGAATGACTAGACTGTCAGCAGAGGATGCAGATGCCCGGCTCCCCAATTCC
 CACGTTGTGTATCAGCTCTGAGCCCTGAGCCTGAGGATGGGGTAGAGGGGAGAGCCTTCCA
 GGTGGACCCCACCTCAGGCAGTGTGACGCTGGGGTGCTCCACTCCGAGCAGGCCAGAAC
 TCCTGCTCTGGTGTGGCCATGGACCTGGCAGGCCAGAGGGTGGCTCAGCAGCACGTG
 GAAGTCGAAGTGCAGTCACAGATATCAATGATCACGCCCTGAGTTCATCACCTCCAGAT
 TGGGCCTATAAGCCTCCCTGAGGATGTGGAGCCGGACTCTGGTGGCCATGCTAACAGCCA
 TTGATGCTGACCTCGAGCCCGCCTCCGCCTCATGGATTTGCCATTGAGAGGGGAGACACA
 GAAGGGACTTTGGCCTGGATTGGGAGCCAGACTCTGGCATGTTAGACTCAGACTCTGCAA
 GAACCTCAGTTATGAGGCAGCTCCAAGTCATGAGGTGGTGGTGGTGCAGAGTGTGGGA
 AGCTGGGGCCAGGCCAGGCCCTGGAGCCACGCCACGGTGAETGTGCTAGTGGAGAGA
 GTGATGCCACCCCCCAAGTGGACCAAGGAGAGCTACGAGGCCAGTGTCCCCATCAGTGC
 AGCCGGCTCTTCTGCTGACCATCCAGCCCTCGACCCATCAGCCGAACCCCTCAGGTCT
 CCCTAGTCATGACTCAGAGGGCTGGCTCTGCATTGAGAAATTCTCCGGGGAGGTGCACACC
 GCCCAGTCCCTGCAGGGGCCAGCCTGGGGACACCTACACGGTGCTTGTGGAGGCCAGGA
 TACAGCCCTGACTCTGCCCTGTGCCCTCCAAATACCTCTGCACACCCGCCAAGACCATG
 GCTTGATCGTGAATGGACCCAGCAAGGACCCGATCTGGCCAGTGGCACGGTCCCTACAGC
 TTCACCCCTGGTCCCAACCCACGGTGCAACGGGATTGGCGCTCCAGACTCTCAATGGTC
 CCATGCCTACCTCACCTGGCCCTGCATTGGTGGAGCCACGTGAACACATAATCCCCGTGG
 TGGTCAGCCACAATGCCAGATGTGGCAGCTCTGGTGCAGTGAAGGGATGCCACGAAGCTGCG
 GTGGAGGGCAGTCATGCGCAAGGTGGCCGATGAAGGGATGCCACGAAGCTGCG
 AGTGGGCATCCTGTAGGCACCCCTGGTAGCAATAGGAATCTCCTCATCCTATTTCACCC
 ACTGGACCATGTCAAGGAAGAAGGACCCGGATCAACCAGCAGACAGCGTGCCCTGAAGGCG
 ACTGTC**TGA**ATGGCCCAGGCAGCTAGCTGGAGCTTGGCCTCTGGCTCCATCTGAGTCCC
 CTGGGAGAGAGGCCAGCACCAAGATCCAGCAGGGACAGGACAGAGTAGAAGCCCCTCCAT
 CTGCCCTGGGTGGAGGCACCATCACCACATCACCAGGCATGTCAGAGCCTGGACACCAAC
 TTTATGGACTGCCATGGAGTGCTCAAATGTCAGGGTGTGTTGCCAATAATAAGCCCCA
 GAGAACTGGCTGGCCCTATGGAAAAAAGAAAAAAGAAAAAAG

FIGURE 132

MVPAWLWLLCVSVPQALPKAQPAELSVEVPENYGGNFPLYLTKLPLPREGAEGQIVLSGDSG
 KATEGPFAMDPDSGFLLVTRALDREEQAQYQLQVTLEMQDGHVLWGPQPVLHVKDENDQVP
 HFSQAIYRARLSRGTRPGIPFLFLEASDRDEPGTANSDLRFHILSQAPAQPSPDMFQLEPRL
 GALALSPKGSTS LDHALERTYQLLVQVKDMGDQASGHQATATVEVSIIESTWVSL EPIHLAE
 NLKVLYPHHMAQVHWSGGDVHYHLESHPPGPFEVNAEGNLYVTRELDREAQAEYLLQVRAQN
 SHGEDYAAPPLELHVLMVDENDNPICPPRDPTVSIPELSPPGTEVTRLSAEDADAPGSPNSH
 VVYQLLSPEPEDGVGRAFQVDPTSGSVTLGVPLRAGQNILLVLAMDLAGAEGGFSSTCE
 VEVAVTDINDHAPEFITSQIGPISLPEDVEPGTLVAMLTAIDADLEPAFRIMDFAIERGDTE
 GTFGLDWEPDSGHVRLRICKNLSYEAAAPSHEVVVVVQSVAKLVGPGPGATATVTVLVERV
 M PPPKILDQESYEASVPISAPAGSFLLTIQPSDPISRTLRFSLVNDSEGWL CIEKFSGEVHTA
 QSLQGAQPGDTYTVLVEAQDTALT LAPVPSQYLCTPRQDHGLIVSGPSKDPDLASGHGPYSF
 TLGPNPTVQRDWRLQTLNGSHAYLT LALHWVEPREHIIPVVVSHNAQM WQLLVRVIVCRCNV
 EGQCMRKVGRMKGMPTKLSAVGILVGTVAIGIFLILIFTWMSRKKDPDQPADSVPLKATV

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 762-784

FIGURE 133

CGGGGAC**ATGAGGTGGATACTGTT**CATTGGGCCCTTATTGGGTCCAGCAGTCAGTGCCCCAA
 GAAAAATTGGGGACCAAGTTGAGGATTAATGTCAGAAATGGAGACGAGATCAGCAA
 ATTGAGTCAACTAGTGAATTCAAACAACCTGAAGCTCAATTCTGGAAATCTCCCTCCTCCT
 TCAATCGGCCTGTGGATGTCCTGGTCCCACATGTCAGTCTGCAGGCATTAAATCCTCCTG
 AGATCCCAGGGCTTAGAGTACGCAGTGACAATTGAGGACCTGCAGGCCCTTAGACAATGA
 AGATGATGAAATGCAACACAATGAAGGGCAAGAACGGAGCAGTAATAACTCAACTACGGG
 CTTACCATTCCCTGGAAGCTATTACACAGAGATGGACAAACATTGCCGCAGACTTCCTGAC
 CTGGCGAGGAGGGTGAAGATTGGACATTGTTGAAAACCGGCCGATGTATGTACTGAAGTT
 CAGCACTGGAAAGGCCTGAGGCCGGCGTTGGCTGAATGCAGGCATCCATTCCGAG
 AGTGGATCTCCAGGCCACTGCAATCTGGACGGCAAGGAAGATTGTATCTGATTACCAGAGG
 GATCCAGCTATCACCTCCATCTGGAGAAAATGGATATTTCTTGTGTCCTGTGGCAATCC
 TGATGGATATGTGTATACTCAAACCTCAAACCGATTATGGAGGAAGACGCCTCCGAAATC
 CTGGAAGCTCCTGCATTGGTGTGACCCAAATAGAAACTGGAACGCTAGTTGCAGGAAAG
 GGAGCCAGCGACAACCCCTGCTCGAAGTGTACCATGGACCCCACGCCAATTGGAAGTGG
 GGTGAAATCAGTGGTAGATTTCATCCAAAACATGGAATTCAAGGGCTTCATCGACCTGC
 ACAGCTACTCGCAGCTGCTGATGTATCCATATGGTACTCAGTCAAAGGCCAGATGCC
 GAGGAACCTGACAAGGTGGCGAGGCTTGCGGCAAAGCTCTGGCTCTGTGTCGGCACTGA
 GTACCAAGTGGTCCCACCTGCACCACTGTCTATCCAGCTAGCGGGAGCAGCATGACTGG
 CGTATGACAACGGCATCAAATTGCAATTGACATTGAGAGATACCGGGACCTATGGC
 TTCCCTCTGCCAGCTAACAGATCATCCCCACTGCAAGGGAGACGTGGCTGGGCTGAAGAC
 CATCATGGAGCATGTGCGGGACAACCTCTACT**AGGC**GATGGCTCTGCTCTGTACATTAT
 TTGTACCCACACGTGCAACGCACTGAGGCCATTGTTAAAGGAGCTTTCTACCTGTGAG
 TCAGAGCCCTCTGGTTGTGGAGCACACAGGCCCTGCCAGCCAGCTCCCTGGAGT
 CGTGTGTCCTGGCGGTGCCCCCTGCAAGAACTGGTTCTGCCAGCCTGCTCAATTGGTCTG
 CTGTTTGATGAGCCTTGTCTGTTCTCCTCCACCTGCTGGCTGGCGGCTGCACTC
 AGCATACCCCTCCTGGTGGCATGTCTCTACCTCATTTAGAACCAAAGAACATC
 TGAGATGATTCTCTACCCCTCATCCACATCTAGCCAAGCCAGTGACCTGCTCTGGGCACT
 GTGGGAGACACCACTTGTCTTAGGTGGCTCAAAGATGATGAGAATTCCCTTAATT
 TCGCAGTCTCCTGGAAAATATTCTTGTGAGCAGCAAATCTGTAGGGATATCAGTGAAG
 GTCTCTCCCTCCCTCTCTGTTTTTTTGAGACAGAGTTGCTCTTGTGCTG
 CAGGCTGGAGTGTGATGGCTCGATCTGGCTCACCACAAACCTCTGCCCTGGGTTCAAGCA
 ATTCTCCTGCCTCAGCCTTGTGAGTAGCTGGTTATAGGCGCATGCCACCATGCCCTGGCTA
 ATTTGTGTTTAGTAGAGACAGGGTTCTCCATGTTGGTCAGGCTGGCTCAAACCTCCA
 ACCTCAGGTGATCTGCCCTCTGGCCTCCCAGAGTGCTGGGATTACAGGTGTGAGCCACTG
 TGCCGGGCCGTCCCTCTTTAGGCCTGAATACAAAGTAGAAGATCACTTCTTCAC
 TGTGCTGAGAATTCTAGATACTACAGTTACTCCTCTCTTGTGTTATTCACTGTG
 ACCAGGATGGCGGGAGGGATCTGTGTCAGTGTAGGTACTGTGCCAGGAAGGCTGGGTGAA
 GTGACCATCTAAATTGCAAGGATGGTGAATTATCCCCATCTGCTCTAATGGGCTTACCTCCT
 CTTGCCTTGTGAACTCAAAAGATCTAGGCCTCATCTACAGGTCTAAATCACTCAT
 CTGGCCTGGATAATCTCACTGCCCTGGCACATTCCATTGCTGTGGTGTATCCTGTGTT
 TCCTTGTCTGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT
 TCTGTCTATTGTTGTTGCTTACCAACATGTCTGAAATCTTAACCTCCTGCCAGGATTGACA
 GCATCTGGTGTGCTTATAAGCCAATAATTCAATGTGAAAAAAAAAAAAAAA

FIGURE 134

MRWILFIGALIGSSICGQEKFQGDQVLRINVNGDEISKLSQLVNSNNLKLNFWKSPSSFNR
PVDVLVPSVSLQAFKSFLRSQGLEYAVTIEDLQALLNEDDEMHQNEGQERSNNFNYGAYH
SLEAIYHEMDNIAADFPDLARRVKIGHSFENRPMYVLKFSTGKVRRPAVWLNAIHSREWI
SQATAIWTAKEKIVSDYQRDPAITSILEKMDIFLLPVANPDGYVYTQTQNRLWRKTRSRNPGS
SCIGADPNRNWNASFAGKGASDNPCSEVYHGPHANSEVEVKSVDIFIQKHGNFKGFIDLHSY
SQLLMYPYGVKKAPDAEELDKVARLAAKALASVSGTEYQVGPTCTTVYPASGSSIDWAYD
NGIKFAFTFELRDTGTYGFLLPANQIIPPTAEETWLGLKTIMEHVRDNLY

Signal peptide:

amino acids 1-16

FIGURE 135

FIGURE 136

MASLYGVLFAVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVSLNTDFAFRLYRRLVLE
TPSQNIFSPSVSVTSLAMLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVP
SKDLTLKMGSALFKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGK
VVDDIIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAF
GVDTELNCFVLQMDYKGDAVAFFVLPSKGKMRQLEQALSARTLIKWSHSLQKRWIEVFIPRF
SISASYNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTT
KFIVRSKDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:

amino acids 1-20

FIGURE 137

FIGURE 138

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 510-532

FIGURE 139

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTGCATCCTCCGACCTTC
 CCAGCAATATGCATCTTGCACGTCTGGTCGGCTCCTGCTCCCTCCTCTGCTACTGGGGGCC
 CTGTCTGGATGGCGGCCAGCGATGACCCCATTGAGAAGGTATTGAAGGGATCAACCGAGG
 GCTGAGCAATGCAGAGAGAGAGGTGGCAAGGCCCTGGATGGCATAACAGTGGAATCACGC
 ATGCCGGAAGGAAAGTGGAGAAGGTTTCAACGGACTTAGCAACATGGGAGCCACACCGGC
 AAGGAGTTGGACAAAGCGTCCAGGGCTCAACCACGGCATGGACAAGGTTGCCATGAGAT
 CAACCATGGTATTGGACAAAGCAGGAAAGGAAGCAGAGAAGCTGGCCATGGGTCAACACG
 CTGCTGGACAGGCCGGGAAGGAAGCAGACAATGCAGTCCAAGGGTCCACACTGGGTCCAC
 CAGGCTGGGAAGGAAGCAGAGAAACTTGGCAAGGGTCAACCAGCTGCTGACCAGGCTGG
 AAAGGAAGTGGAGAAGCTTGGCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGC
 TGCAGAATGCTCATAATGGGTCAACCAAGCCAGCAAGGAGGCCAACAGCTGCTGAATGGC
 AACCATCAAAGCGGATCTCCAGCCATCAAGGAGGGCCACAACCACGCCGTTAGCCTCTGG
 GGCTCAGTCAACACGCCCTTCATCAACCTTCCGCCCTGTGGAGGAGCGTCGCCAACATCA
 TGCCCTAAACTGGCATCCGGCTTGCTGGAGAATAATGTCGCCGTTGTCACATCAGCTGAC
 ATGACCTGGAGGGTTGGGGACAGGTTCTGAAATCCCTGAAGGGGGTTGTACTG
 GGATTGTGAATAACTGATAACACCA

FIGURE 140

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITAG
REVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAG
QAGKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQN
AHNGVNQASKEANQLLNGNHQSGSSSHQGGATTPLASGASVNTPFINLPALWRSVANIMP
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

FIGURE 141

CTCCGGGTCCCCAGGGGCTGCGCCGGGCCCTGGCAAGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
 CCCGCGGGGGCGATGACCGTGCCTGACCCCTGACTCACTCCAGGTCCGGAGGCAGGGGCCCCCGGGGCGACTCG
 GGGCGGACCGCGGGCGGAGCTGCCGCCGTGAGTCGGCCGAGCCACCTGAGCCCCGAGCCGGGACACCGTC
 GCTCCTGCTCTCCGA**ATG**CTGCGCACCGCGATGGGCCCTGAGGAGCTGGCTCGCCGCCCATGGGGCGCGCTGCCG
 CCTCGGCCACCGCTGCTGCTCCTGCTGCTGCTCCTGCTGCAGCCGCCGCCCTCGACCTGGGCGCTCAGC
 CCCCAGATCAGCCTGCCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTGAAGCTGAACACATCTCAAAC
 ACAGCCCTCTGCTGAGCAGGGATGGCAGGACCTGTACGTGGGTGCTCGAGAGGCCCTTTGCACTCAGTAGC
 AACCTCAGCTCCTGCCAGGGGGAGTACCAAGGAGCTGCTTGGGTGAGACGAGAAGAAACAGCAGTC
 AGCTTCAAGGGCAAGGACCCACAGCGCACTGTCAAAACTACATCAAGATCCTCCTGCCCTCAGCGCAGTC
 CTGTCACCTGTGGCACAGCAGCCTCAGCCCCATGTGACCTACATCAACATGGAGAACTTCACCCCTGGCAAGG
 GACGAGAAGGGGAATGTCCTCTGGAGAGATGGCAAGGGCGTTGTCCTTGACCCGAATTCAAGTCCACTGCC
 CTGGTGGTTGATGGCGAGCTACACTGGAACAGTCAGCAGCTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
 CAAAGCCTTCGCCCAACAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTGTGGCCTCAGCCTAC
 ATTCTGAGAGCCTGGCAGCTTGCAAGGCAGTGTGACAAGATCTACTTTTCTCAGCAGACTGGCAGGAA
 TTTGAGTTCTTGAGAACACCATTGTGCTCCCGCATTGCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
 CTACAGCAGCCTGCCACCTCTCAAGGCCAGCTGCTGCTCACGGCCGACGATGGCTCCCCCTCAAC
 GTGCTGAGGATGTCCTCACGCTGAGCCCCAGCCCCAGGACTGGCGTACACCTTTCTATGGGGTCTTC
 TCCCAGTGGCACAGGGAAACTACAGAAGGCTCTGCCGCTGTGCTTCAATGAAGGATGTGAGAGACTTC
 AGCGGCCTCTACAAGGAGGTGAAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGC
 CCTGGGAGCTGATCACCAACAGTGCCGGGAAAGGAAGATCAACTCATCCCTGAGCTCCCAGACCGCGTGC
 AACCTCCTCAAGGACCACTTCCTGATGGACGGCAGGTCCGAAGCCGATGCTGCTGAGCCCCAGGCTCG
 TACCAAGCCGCTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCCTCTTCTGGCACTGGTAC
 GGCCGGCTCCACAAGGAGGTGAGCGTGGGGGGGGTGCACATATTGAGGGAGCTGAGATCTCTCATCGGA
 CAGCCCGTGCAGAACTGCTCTGGACACCCACAGGGGGCTGCTGTATGGGGCTCACACTCGGGCGTAGTCCAG
 GTGCCCATGGCCAACCTGAGCCTGTACGGAGCTGTTGGGACTGCTCTCGCCGGGACCCCTACTGTGCTTGG
 AGCGGCTCCAGCTGAAAGCACGTCAGCCTCTACACGCTCAGCTGGCCACCAGGGCTGGATCCAGGACATCGAG
 GGAGCCAGCCAAGGACCTTGCAGCGCTCTCGGTTGTGCCCCGTCTTGTACCAACAGGGAGAAAGCCA
 TGTGAGCAAGTCCAGTCCAGCCAAACACAGTGAACACTTGGCTGCCCTCCTCTCAACCTGGCAGCCGA
 CTCTGGCTACGCAACGGGCCCCGTCAATGCCCTGGCCTCTGCCACGTGCTACCCACTGGGACCTGCTGCTG
 GTGGGACCCAACAGCTGGGGAGTTCCAGTGTGCTGACTAGAGGAGGGCTCCAGCAGCTGGTAGCCAGCTAC
 TGCCCAGAGGTGGTGGAGGACGGGTGGCAGACCAAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
 TCGCGTGTGAGTCACCAGCTGGTGGCAAGGCCAGTGGGTGCAAGACAGGTCTACTGGAAGGAGTTCTGGTG
 ATGTGCAAGCTTTGTGCTGCCGTGCTGCTCCAGTTATTCTGCTCACCGGCACCGGAACAGCATGAAA
 GTCTCCCTGAAGCAGGGGGAAATGTGCCAGCGTGCACCCCAAGACCTGCCCTGGTGCTGCCCTGAGACCCGC
 CCACTCAACGGCTAGGGCCCCCTAGCACCCGCTCGATCACCGAGGGTACAGTCCCTGTCAGACAGCCCCCG
 GGGGGCCGAGCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTGTGGAGGTATCCCCAGTG
 TGCCCCGGGGGGGGTCCGCCCTGGCTGGAGATCCGTGACTCTGTGGGT**G**AAGAGCTGACTTCCAGAGGACGC
 TGCCCTGGCTTCAAGGGCTGTGAATGTCGGAGAGGGTCAACTGGACCTCCCTGCCCTGCTGCTCTCGTGG
 ACGACCGTGGTGCCGGCCCTGGAGGCCAGCTGGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
 TACCAACAGACACCCAAACAGCGTGGCCCCAGAGGTCTGCCAAATATGGGGCTGCCTAGGTGGTGAA
 CAGTGTCTTATGTAAACTGAGCCCTTGTGTTAAAAAAATCTAAATGTGAAACTAGAATGAGAGGGAGAG
 ATAGCATGGCATGCAGCACACAGGCTGCCAGTTCACTGGCTCTTCACTTCCACATTATCCGCTGCCACCGGCTGC
 TTGCTGAGACAGAGTGGAAACCCCTACCAACTGGCTCTGCCAGTGCAGCCAGGGATGTAGTT
 CCTGTCTACTGCAGATTCAAGGACCACTGAGGCTAGGTGGCACTGCCCTCACCAAGGTCTGGGCTC
 TTGCTGCCGTGCTCCACCACTCAGGGACCAAGAGGGCTAGGTGGCACTGCCCTCACCAAGGTCTGGGCTC
 GGACCCAACCTCTGGACCTTCCAGCCTGATCACGGCTGTGGCCACACAGAGGAGACAGCGCGAGCTCAGGAGAGA
 TTTCGTGACAATGTACGCCCTTCAGAATTCAAGGGAGAGACTGTCGCCCTGCCCTCTCGTTGTGCGTGA
 GAACCCGTGTGCCCTTCCCACCATATCCACCCCTGCCATCTTGAACCTCAAACACGAGGAACACTAAC
 CTGGTCTCTCCCCAGTCCCCAGTTCACCCATCCACCTCCACTCTAAGGGATATCAACACTGCC
 AGCACAGGGCCCTGAATTATGTGGTTTATACATTAAATAAGATGCACTTATGTCATTAAATAAAA
 GTCTGAAGAATTACTGTTAAAAAAAAAAAAA

FIGURE 142

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPLLLLLLQLQQPTWALSPRISLPLGSEERPFLRF
EAEHISNYTALLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEKKQQCSFKG
KDPQRDCQNYIKILLPLSGSHLFTCGTAAFSPMCTYINMENFTLARDEKGNVILLEDGKGRCP
FDPNFKSTALVVDGELYGTVSSFQGNDPAISRSQLRPTKTESSLNWLDPAFVASAYIPE
SLGSLQGDDDKIYFFFSETGQEFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLC
SRPDDGFNFNVLQDVFTLSPSPQDWRTDLFYGVFTSQWHRGTTEGSACVFTMKDVQRVFSG
LYKEVNRETQQWYTWTVPPTPRPGACITNSARERKINSSLQLPDRVLNFLKDHFLMDGQVR
SRMLLQLPQARYQRVAVHRVPGLHHTYDVLFLGTGDGRHLHAVSVGPRVHIEELQIFSSGQ
PVQNLLLDTHRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLYQP
QLATRPWIQDIEGASAKDLCASSVVSPSFVPTGEKPCEQVQFQPNTVNTLACPLLSNIATR
LWLRNGAPVNASASCHVLPTGDLVVGTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQ
TDEGGSPVIIISTSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSM
KVFLKQGECASVHPKTCPVVLPPETRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTESERK
PLSIQDSFVEVSPVCPRPRVRLGSEIRDSVV

```

Transmembrane domains:

amino acids 23-46 (type II), 718-738

FIGURE 143A

CTAAGCCGGAGGATGTGCAGCTGCCGCCGCCGCGCCGGCTACGAAGAGGACGGGGACAGGCGCCGTGCGAACCGA
 GCCCAGCCAGCCGGAGGACGCCGCCAGGGCGGGACGGGAGCCGGACTCGTCTGCCGCCGTGCGCGCTCG
 TGCCGGCCCCCGCTCCCCGCCGCCAGCGGGAGGAGCCGCCACCTCGGCCCGAGGCCGCCGTAGCGCCGCC
 CGGGCATGGTCCCCCTTTAAAGGCGCAGGCCGCCGCCGGGGCGGTGCGGAACAAAGCGCCGCCGCC
 CCTGCAGGGCGGCTCGGGGCCGATGGCGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC
 CGCGCTAGGGCGGGCTGGCTCCGTGGCGGGGCCAGCGGGCTGAGGGCGCGAGCCTGCCGCCGCC
 GGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC
 ATGGCGCGGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC
 TGCTCGGGCTCGTCTGGCTCGTCTGGCTCGGCCGCTGTCCTGCCCGGGCTTCCGAGCTGAAGCGAGCGG
 GCCCACGGCGCCGCCAGCCCAGGGCTGCCGTCCGGCAGGCCGCCGCCGCCGCCGCC
 GCGATGCCGCCGGGGCGCAGCTCTGGCCGCCGCCGCCGCCGCCGCCGCC
 TCGTGGGAGTCATGACGCCAGAAATACTGCAGACTCGGGCGTGGCCGCCTACAGAACATGGTCCAAGACAA
 TTCTGGAAAGTTCAGTTCTCAAGTGAGGGTCTGACACATCTGTACCAATTCCAGTAGTGCCACTACGGG
 GTGTGGACGACTCCTACCCGCCAGAAGAAGTCCTCATGATGCTCAAGTACATGCACGACCAACTTGGACA
 AGTATGAATGGTTATGAGAGCAGATGATGACGTGACATCAAAGGAGACCGTCTGGAGAACTTCTGAGGAGTT
 TGAACAGCAGCGAGCCCTTTCTGGCAGACAGGCCCTGGCACCACGGAAGAAATGGAAAATGGCCCTGG
 AGCCTGGTGAGAACCTCTGCATGGGGGCCCTGGCGTATGAGCCGGAGGTGCTTCGGAGAATGGTGCCGC
 ACATTGGCAAGTGTCTCGGGAGATGTACACCACCCATGAGGACGTGGAGGTGGGAAGGTGTCCGGAGGTTG
 CAGGGGTGCAAGTGTGTCTGGCTTATGAGATGCGCAGCTTTTATGAGAAATTACGAGCAGAACAAAAAGGGT
 ACATTAGAGATCTCCATAACAGTAAACATCAGGAGCTATCACATTACACCCAAACAAAAACCCACCCCTACCAAGT
 ACAGGCTCCACAGCTACATGCTGAGGCCAAGATATCCGAGCTCCGCCATCGCACAATACAGCTGCACCGCGAAA
 TTGCTCTGATGAGCAAATACAGCAACACAGAAATTCTAAAGAGGACCTCAGCTGGGAATCCCTCCCTCCTCA
 TGAGGTTTCAGCCCCGCCAGCGAGGGAGATTCTGGAAATGGAGTTCTGACTGGAAAATACTTGTATTGCGCAG
 TTGACGGCCAGCCCCCTCGAAGAGGAATGGACTCCGCCAGAGGGAAAGCCTTGGACGACATTGTCATGCAGGTCA
 TGGAGATGATCAATGCCAACGCAAGACCGAGGGGCCATATTGACTCAAAGAGATCCAGTACGGCTACCGCC
 GGGTGAAACCCATGATGGGCTGAGTACATCCTGGACCTGCTGTTCTGTCACAAAAGAACAGCACAAGGGAAAGAAA
 TGACGGTCCCTGTGAGGAGGCACGCGTATTTACAGCAGACTTCAGCAAATCCAGTTGTGGAGCATGAGGAGC
 TGGATGCAAAAGAGTTGGCAAGAGAAATCAATCAGGAATCTGGATCCTGCTTCTCTCAAACCTCCGTGAAGA
 AGCTCGTCCCCCTTCAGCTCCCTGGTCAAGAGTGTGAGCACAAGAACCAAAGATAAAAGATAAACATACTGA
 TTCTTTGCTGGCGTTGACATGTTGTGAGATTATGGAAAATTTGAGAAGACGTGTCTTATCCCCAATC
 AGAACGTCAGCTCGTGGTCTGCTTCAATTCTGACTCCAACCCCTGACAAGGCCAAACAAGTGAACGTGATGA
 GAGATTACCGCATTAAAGTACCCCAAAGCCGACATGCAAGATTTGCTGTGCTGGAGAGTTTCAAGAGGCCCTGG
 CCCTGGAAAGTAGGATCCTCCAGTTAACATGAATCTTGTCTTCTGCGACGTCGACCTCGTGTACTA
 CAGAACATTCTCAGCGATGTCGAGCAAATACAGTTCTGGCCAACAAATATATTTCCAATCATCTCAGCCAGT
 ATGACCCAAAGATTGTTATAGGGAAAGTCCCAGTGACAACCATTGCTTTACTCAGAAAACGGCTTCT
 GGAGAAAATATGGTTTGGCATCACGTGATTTATAAGGGAGATCTTGTCCAGTGGGGCTTGATGTTCCA
 TCCAAGGCTGGGGCTGGAGGATGTGGACCTTTCAACAAGGTGTCCAGGCAAGGTTGAAGACGTTAGGAGCC
 AGGAAGTAGGAGTAGCCACGCCATCTGTCTTGTGATCCAACTTGTGACCCAAACAGTACAAAATGT
 GCTTGGGCTCAAAGCATCGACCTATGGGCCACCCAGCAGCTGGCTGAGATGTGGCTGGAAAAAAATGATCCAA
 GTTACAGTAAAAGCAGCAATAATGGCTCAGTGAGGACAGCCTAATGTCCAGTTGCTGGAAAAGACGTTT
 TAATTATCTAATTATTGTTCAAAATTTGTTGATGTCAGTTGAGTCTGCTGTTACAGTGTGAACTTGTGAA
 AAGTGGTTTCTTACATAGGACTCTTAAAGATTGAGCTTCTGAAACAAGAAGGTGATCAGTGTGCTTGGCTTGA
 CACATCTCTGCTGAACATTATGTCAGCAGACCTGCTTAACCTTGTGAAATGTACCTGATGAACAAAATTT
 TTTAAAAAAATGTTTCTTGTGAGACCTTGTCTCAGTCCTATGGCAGAAAACGTGAACATTCTGCAAAGTAT
 TATTGTAACAAAACACTGTAACCTGGTAAATGTTGTGATTGTTAACATTCCACAGATTCTACCTTTGT
 GTTTGTTTTTTTACAATTGTTAAAGCCATTGTCAGTTGAGATAAGGAAATGTGATAATA
 GCTGTTCATCTGCTTCAGGAGAGCTTCCAGAGGTGATCATTCTCTCATGGTACTCTGCTCAGCATGGC
 CACGTAGGTTTTTGTGTTGTTGTTCTTGTGAGACGGAGTCTCACTCTGTTACCCAGGCTGGAAATG
 CAGTGGCGCAATCTGGCTCACCTAACCTCCACTTCCCTGGTCAAGCAATTCCCTGCCCTCCGAGT
 AGCTGGGATTACAGGCACACACCACGCCAGNTAGTTTTGTATTTTAGTAGAGACGGGGTTTACCAT
 GCAAGCCCAGCTGCCACGTAGTTAAAGCAAGGGCGTGAAGAAGGCACAGTGAGGTATGTGGCTGTTCTCG
 TGGTAGTTCATCGGCCCTAAATAGACCTGGCATTAAATTCAAGAAGGATTGGCATTCTCTTCTGACCTT
 CTCTTAAAGGGTAAATATTAAATGTTAGAATGACAAGAGATGAATTATTACAATAATCTGATGACACAGACT
 GAAACATACACACATACACCCCTAACAAACGTTGGGAAAATGTATTTGTTGTTCTGAAATACCTTAA
 TTTATTTAATATCTGTTGTTCAAGAGCTGCCCCATTTCTGAGTACCTGTTAGTTAGTATTATTTATGTGATCGG
 GAGTGTGTTAGTGTGTTATTGCACTAAACGATCTCCAAAGATTTCTTGGAAACGCTTTCCCCCTCC

FIGURE 143B

TTAATTTTATATTCTTACTGTTACTAAATATAAGTGTCTTGACAATTGGTGCTCATGTGTTGGG
GACAAAAGTGAATGAATCTGTCATTATACCAGAAAGTTAAATTCTCAGATCAAATGTGCCTTAATAAATTGTT
TTCATTTAGATTCAAACAGTGATAGACTGCCATTAAATACACGTATTGGAGGGCTGCGTATTTGTAATAG
CCTGATGCTATTGGAAAAAAACCAAGTGAACAATATTTCTATTGACTTTCGAACCAACCGATTGTCTCATT
ATTCCCTGTTTAGCTGAAGAATTGTATTACATTGGAGAGTAAAAACTAAACACGAAAAAA

FIGURE 144

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68836
><subunit 1 of 1, 802 aa, 1 stop
><MW: 91812, pI: 9.52, NX(S/T): 3
MAARGRRAWSVLLGLVLGFVLASRLVLPRASELKAGPRRRASPEGCRSGQAAASQAGGAR
GDARGAQLWPPGSDPDGGPRDRNFLFVGVMTAQKYLQTRAVAAYRTWSKTIPGVQFFSSEG
SDTSVPVIPVVPLRGVDDSYPPQKKSFMMLKYMHDHYLDKYEFMRADDDVYIKGDRLENFLR
SLNSSEPLFLGQTGLGTTEEMGKLALEPGENFCMGGPGVIMSREVLRRMVPHIGKCLREMYT
THEDVEVGRCVRRFAGVQCVWSYEMRQLFYENYEQNKKGYIRDLHNSKIHQAITLHPNKNPP
YQYRLHSYMLSRKISELRHRTIQLHREIVLMSKYSNTEIHKEDEQLGIPPSFMRFQPRQREE
ILEWEFLTGKYLYSAVDGQPPRRGMDSAQREALDDIVMQVMEMINANAKTRGRIIDFKEIQY
GYRRVNPMPYGAEYILDLLLLYKKHKKGKMTVPVRRHAYLQQTFSKIQFVEHEELDAQELAKR
INQESGSLSFLSNSLKKLVPFQLPGSKSEHKEPKDKKINILIPLSGRFDMFVRFMGNFEKTC
LIPNQNVKLVLLLNSDSNPDKAKQVELMDYRIKYPKADMQILPVSGEFSRALALEVGSSQ
FNNESLLFFCDVDLVFTTEFLQRCRANTVLGQQIYFPIIFSQYDPKIVYSGKVPSDNHFAFT
QKTGFWRNYGFGITCIYKGDLVRVGGFDVSIQGWGLEVDLFNKVVQAGLKTFRSQEVGVVH
VHHPVFCDPNLDPKQYKMCLGSKASTYGSTQQLAEMWLEKNDPSYSKSSNNNGSVRTA
```

Signal peptide:

amino acids 1-23

FIGURE 145

GGACAACC GTT GCT GGG GTCC AGGG CCT GAGG CAGG AC GG TACT CCG CT GAC AC CCT CCC
 TT CGGC TT GAGG TT CC AGC CT GG TGCC CCA AGG AC GT CC GG CG AT GG CAG AGT GCT
 ACGG AC GAC GC CT **ATGAAGCC** TAGC CTT CTAG TT GCG CTT GCT AT GG CTT CGT CTG
 TGCC GG CT TAT CC GAG CATA ACT GT GAC AC CT GAT GAAG AGC AAA ACT TGA AT CATT ATATA
 CAAG TTT AGAGA AAC CTAG TAC GAAG TGT CCCT CTGGG AGCC AGGT CGT GAGAAAAA ATC
 TA ACT CT CCAAA ACAT GTT ATT CTAT AGCAT CAA AGGG ATCAA ATT AAGG AGCT AGTTA
 CAC AT GGAG AC GCT TCA CT GAGA AT GAT GTT TA ACCA AT CCT AT CAGT GAAG AA ACT ACA
 ACT TT CCCT ACAGG AGG CTTC ACAC CGG AA ATAGG AA AGAAAAA ACAC CGG AA AGT ACCCC
 ATT CT GG TCG AT CAA ACCA AA CAAT GTT CCATT GTT GAT GCAG AGGA ACCT TAT ATT G
 AAA AT GAAG AGCC AGAG CCAG AGCC CGAG GCG AGCC AGCT GCAAA AC AA ACT GAGG CACCA AGA ATG
 TTGCCAGTTGTTACTGAATCATCTACAAGTCCATATGTTACCTCATACAAGTCACCTGTCAC
 CACTT TAGATAAGAGCACTGGCATTGAGATCTCTACAGAATCAGAAGATGTTCCCTCAGCTCT
 CAGGTGAAACTGCGATAGAAAAACCGAAGAGTTGGAAAGCACCCAGAGAGTTGGAATAAT
 GATGACATTTGAAAAAAATTAGATATTAATT CACAAGTGCAACAGGCAC TTCTTAGTGA
 CACCAGCAACCCAGCATATAGAGAAGATATTGAAGCCTCTAAAGATCACCTAAAAGCAAGCC
 TTGCTCTAGCAGCAGCAGCAGAACATAAATTAAAAACAATGTATAAGTCCCAGTTATTGCCA
 GTAGGACGAACAAGTAATAAAATTGATGACATCGAAACTGTTATTACATGCTGTGTAATT
 TAGATCTAAACTCTATGAATATTAGATATTAAATGTGTTCCACCAGAGATGAGAGAAAAAG
 CTGCTACAGTATTCAATACATTAAAAATATGTGTAAGATCAAGGAGAGTCACAGCCTTATTA
 AAAGTTTAT**TAA**ACAATAATATAAAATTAAACCTACTTGATATTCCATAACAAAGCTGA
 TTTAAGCAAAC TGCA TTTT CACAGG AGAA ATAATC ATATT CGTA ATT CAAAAGTTGTAT
 .AAAAAATATTCTATTGATGTTCAAATGTGCCAACATCTTATGTGTCATGTGTTATGAACA
 ATTTCATATGCACTAAAAACCTAATTAAAATTTGGTTCAAGGAAAAAA

FIGURE 146

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68864
><subunit 1 of 1, 350 aa, 1 stop
><MW: 39003, pI: 5.59, NX(S/T): 1
MKPLVILLVALLWPSSVPAYPSITVTPDEEQNLNHYIQVLENLVRSPSGEPGREKKNSPK
HVYSIASKGSKFKELVTHGDASTENDVLNPISEETTFPTGGFTPEIGKKKTESTPFWSI
KPNNVSIVLHAEPYIENEPEPEPAAKQTEAPRMLPVVTESSTSPYVTSYKSPVTTLDK
STGIEISTESEDVPQLSGETAIEKPEEFGKHPESWNNDDILKKILDINSQVQQALLSDTSNP
AYREDIEASKDHLKRSLALAAAAEHKLKTMYKSQLLPVGRTSNKIDDIEVTINMLCNSRSKL
YEYLDIKCVPPEMREKAATVFNTLKNMCRSRRVTALLKVY
```

Signal peptide:

amino acids 1-19

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19

FIGURE 147

CGGCTCGAGC GGCTCGAGTGAAGAGCCTCTCCACGGCTCCTGCGCCTGAGACAGCTGGCCTG
 ACCTCCAAATCATCCATCCACCCCTGCTGCATCTGTTTCATAGTGTGAGATCAACCACA
 GGAATATCC**ATG**GCTTTGTGCTCATTGGTTCTCAGTTCTACGAGCTGGTGTAGGACA
 GTGGCAAGTCACTGGACGGGCAAGTTGTCAGGCCCTGGTGGGGAGGACGCCGTGTTCT
 CCTGCTCCCTCTTCCTGAGACCAGTGCAGAGGCTATGGAAGTGCGGTTCTCAGGAATCAG
 TTCCATGCTGTGGTCCACCTCTACAGAGATGGGGAAAGACTGGGAATCTAAGCAGATGCCACA
 GTATCGAGGGAGAACTGAGTTGTAAGGACTCCATTGCAGGGGGCGTGTCTCTAAGGC
 TAAAAAAACATCACTCCCTCGGACATCGGCTGTATGGGTGCTGGTTCAGTTCCAGATTAC
 GATGAGGAGGCCACCTGGGAGCTGCGGGTGGCAGCACTGGGCTCACTCCTCTCATTCCAT
 CGTGGGATATGTTGACGGAGGTATCCAGTTACTCTGCCTGTCCTCAGGCTGGTCCCCCAGC
 CCACAGCCAAGTGGAAAGGTCCACAAGGACAGGATTGTCAGACTCCAGAGCAAATGCA
 GATGGGTACAGCCTGTATGATGTGGAGATCTCATTATAGTCCAGGAAAATGCTGGAGCAT
 ATTGTGTTCCATCCACCTTGCTGAGCAGAGTCATGAGGTGGAATCCAAGGTATTGATAGGAG
 AGACGTTTTCCAGCCCTCACCTGGCGCCTGGCTTCTATTAACTCGGGTTACTCTGTGGT
 GCCCTGTGTGGTGTGTCATGGGATGATAATTGTTCTCAAATCCAAGGGAAAATCCA
 GGCAGGAACGGACTGGAGAAGAACGACGGACAGGAGAAATTGAGAGACGCCCGAAACACG
 CAGTGGAGGTGACTCTGGATCCAGAGACGGCTCACCGAAGCTCTGCGTTCTGATCTGAAA
 ACTGTAACCCATAGAAAAGCTCCCCAGGAGGTGCCTCACTCTGAGAAGAGATTACAAGGAA
 GAGTGTGGTGGCTCTCAGGGTTCCAAGCAGGGAGACATTACTGGGAGGTGGACGTGGAC
 AAAATGTAGGGTGGTATGTGGAGTGTGCGGATGACGTAGACAGGGGAAGAACATGTG
 ACTTTGTCTCCCAACAATGGGTATTGGGTCTCAGACTGACAACAGAACATTGTATTTCAC
 ATTCAATCCCCATTATCAGCCTCCCCCCCAGCACCCCTCTACACGGAGTAGGGTCTTCC
 TGGACTATGAGGGTGGGACCATCTCCTCTCAATACAAATGACCAGTCCCTATTATACC
 CTGCTGACATGTCAGTTGAAGGCTTGTGAGACCCATATCCAGCATGCGATGTGACGA
 GGAAAAGGGACTCCCATTATCATATGTCCAGTGTCTGGGG**TGA**GACAGAGAACCCCTG
 CTTAAAGGGCCCCACACCCACAGACCCAGACACAGCAAGGGAGGTGCTCCGACAGGTGGC
 CCCAGCTCCTCTCCGGAGCCTGCGCACAGAGACTCACGCCCTACTCTCCTTAGGGAGC
 TGAGGTTCTCTGCCCTGAGCCTGCAAGCAGGGAGTCACAGCTTCAGATGAGGGGGAT
 TGGCCTGACCTGTGGGAGTCAGAAGCCATGGCTGCCCTGAAGTGGGGACGGAAATAGACTCA
 CATTAGGTTAGTTGTAAAACCTCCATCCAGCTAAGCGATCTTGAACAAGTCACAACCTCC
 CAGGCTCCTCATTTGCTAGTCACGGACAGTGATTCTGCCTCACAGGTGAAGATTAAAGAGA
 CAACGAATGTGAATCATGCTTGCAAGGTTGAGGGCACAGTGTGCTATTCCACATTAATTACTTTCTA
 TATTATACATTTCCCACCAAAACTCTGTTGCTATTCCACATTAATTACTTTCTA
 TACCAAATCACCCATGGAATAGTTATTGAAACACCTGCTTGTGAGGCTCAAAGAATAAGAG
 GAGGTAGGATTTCACTGATTCTATAAGCCCAGCATTACCTGATACAAAACCAGGCAAAG
 AAAACAGAAGAAGAGGAAGGAAAACATCAGGTCCATATCCCTCATTAACACAGACACAAAAA
 TTCTAAATAAAATTAAACAAATTAAACTAAACAAATTATTAAAGATGATATATAACTACT
 CAGTGTGGTTGTCCCACAAATGCAGAGTTGGTTAATATTAAATATCAACCAGTGTAAATT
 CAGCACATTAAATAAGTAAAAAGAAAACCATAAAAAAAAAAAAAAA

FIGURE 148

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68866
><subunit 1 of 1, 466 aa, 1 stop
><MW: 52279, pI: 6.16, NX(S/T): 2
MAFVLILVLSFYELVSGQWQVTGPGKFKVQALVGEDAVFSCSLFPETSAEAMEVRFFRNQFHA
VVHLYRDGEDWESKQMPQYRGRTEFKDSIAGGRVSLRLKNITPSDIGLYGCWFSSQIYDEE
ATWELRVAALGSLPLISIVGYVDGGIQLLCLSSGWFQPPTAKWKGPQGQDLSSDSRANADGY
SLYDVEISIIVQENAGSILCSIHLAEQSHEVESKVVLIGETFFQPSPWRLASILLGLLCALC
GVVMGMIIVFFKSKGKIQAELDWRRKHGQAEILDARKHAVEVTLDPETAHPKLCVSDLKTVT
HRKAPQEVPHSEKRFRTRKSVVASQGFQAGRHYWEVDVGQNVGWYVGVCRDDVDRGKNNVTLS
PNNGYWVLRLTTEHLYFTFNPHFISLPPSTPPTRGVFLDYEGGTISFFNTNDQSLIYTLLT
CQFEGLLRPYIQHAMYDEEKGTPIFICPVSWG
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 131-150, 235-259

FIGURE 149

CCTTCACAGGACTCTCATTGCTGGTTGGCA**ATG**ATGTATCGGCCAGATGTGGTGAGGGCTA
 GGAAAAGAGTTGTTGGAACCCCTGGTTATCGGCCTCGTCATCTTCATATCCCTGATTGTC
 CTGGCAGTGTGCATTGGACTCACTGTTATTATGTGAGATATAATCAAAAGAACACTACAA
 TTACTATAGCACATTGTCATTACAACGTACAAACTATATGCTGAGTTGGCAGAGAGGCTT
 CTAACAATTTACAGAAATGAGCCAGAGACTTGAATCAATGGTAAAAATGCATTTATAAA
 TCTCCATTAAGGGAAGAATTGTCAAGTCTCAGGTTATCAAGTTCAAGCAGAACAGCATGG
 AGTGTGGCTCATATGCTGTTGATTGTAGATTCACTCTACTGAGGATCCTGAAACTGTAG
 ATAAAAATTGTTCAACTTGTACATGAAAAGCTGCAAGATGCTGTAGGACCCCCCTAAAGTA
 GATCCTCACTCAGTAAAATTAAAAAAATCAACAAGACAGAACAGACAGCTATCTAAACCA
 TTGCTGCGGAACACGAAGAAGTAAAACCTCTAGGTAGAGTCAGGATCGTTGGTGGACAG
 AAGTAGAAGAGGGTGAATGGCCCTGGCAGGCTAGCCTGCAGTGGATGGAGTCATCGCTGT
 GGAGCAACCTTAATTAAATGCCACATGGCTTGAGTGCTGCTCACTGTTACAACATATAA
 GAACCCCTGCCAGATGGACTGCTCCCTTGGAGTAACAATAAAACCTCGAAAATGAAACGGG
 GTCTCCGGAGAATAATTGTCATGAAAATACAAACACCCATCACATGACTATGATATTCT
 CTTGCAGAGCTTCTAGCCCTGTTCCCTACACAAATGCAGTACATAGAGTTGTCTCCCTGA
 TGCATCCTATGAGTTCAACCAGGTGATGTGATGTTGTGACAGGATTGGAGCACTGAAAA
 ATGATGGTTACAGTCAAAATCATCTCGACAAGCACAGGTGACTCTCATAGACGCTACAAC
 TGCAATGAACCTCAAGCTTACAATGACGCCATAACTCCTAGAATGTTATGTGCTGGCTCCT
 AGAAGGAAAAACAGATGCATGCCAGGGTACTCTGGAGGACACTGGTTAGTCAGATGCTA
 GAGATATCTGGTACCTTGCTGGAATAGTGAGCTGGGAGATGAATGTGCGAAACCCAACAAG
 CCTGGTGTATTTACTAGAGTTACGGCCTTGGGGACTGGATTACTTCAAAACTGGTATC**TA**
AGAGACAAAAGCCTCATGGAACAGATAACATTGTTGGGTGTGGAGGCCATT
 TTTAGAGATAACAGAATTGGAGAAGACTTGCAAAACAGCTAGATTTGACTGATCTAATAAC
 TGTTTGCTGATGCATGTATTTCTCCAGCTCTGTTCCGCACGTAAGCATCCTGCTTCTG
 CCAGATCAACTCTGTCACTGTGAGCAATAGTTGAAACTTATGTACATAGAGAAATAGATA
 ATACAATATTACATTACAGCCTGTATTCTAGAAGTTGTCTAGAAGTTGTCTAGAATTGAC
 TTGTTGACATAAATTGTAATGCATATATAACATTGAAAGCCTCTTCAAGGAGTGAAGAAAATA
 TAAGAAGAAAAAAATCCCCTACATTGAGCAAGAAAAGTATTAGGTGTTTTCTTAGT
 GGAATATTAGAAATGATCATATTGAGCAAGGAGTCAAGCAAAGACAGCAGAACATCAAC
 ACTTCATCATTAGGAAGTATGGAAACTAAGTTAAGGAAGTCCAGAAAGAACAGCAAGATATA
 TCCTTATTTCTTCAACAAACTACTATGATAAATGTGAAGAAGATTCTGTTCTAGAATTTGT
 ACCTATAATAATTACAAACTTCATGCAATGTACTTGTAAAGCAAATTAAAGCAAATAT
 TTATTAAACATTGTTACTGAGGATGTCAACATATAACAAATAAAATAAATCACCCA

FIGURE 150

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68871
><subunit 1 of 1, 423 aa, 1 stop
><MW: 47696, pI: 8.96, NX(S/T): 3
MMYRPDVVRARKRVCWEPWVIGLVIFISLIVLAVCIGLTVHYVRYNQKKTNYYSTLSFTTD
KLYAEFGREASNNFTEMSQRLESMVKNAYKSPLREEFVKSQVIKFQQKHGVLAHMLLICR
FHSTEDPETVDKIVQLVLHEKLQDAVGPPKVDPHSVKIKKINKTETDSYLNHCCGTRRSKTL
GQSLRIVGGTEVEEGEWPWQASLQWDGSHRCGATLINATWLVSAAHCFTTYKNPARWTASFG
VTIKPSKMKRGLRRIIVHEKYKHPHDYDISLAELOSSPVPTNAVHRVCLPDASYEFQPGDV
MFVTGFGALKNDGYSQNHLRQAQVTLIDATTNEPQAYNDAITPRMLCAGSLEGKTDACQGD
SGGPLVSSDARDIWYLAGIVSWGDECAKPNKPGVYTRVTALRDWITSKTI
```

Transmembrane domain:

amino acids 21-40 (type II)

FIGURE 151

GTCGAAGGTTATAAAAGCTTCCAGCAAACGGCATTGAAGTTGAAGATAAACCTGACAGCA
 CAGCCTGAGATCTGGGATCCCTCAGCCTAACACCCACAGACGTAGCTGGTGGATTCCCG
 CTGCATCAAGGCCTACCCACTGTCTCC**ATG**CTGGGCTCTCCCTGCCTCTGTGGCTCCTGGC
 CGTGACCTTCTGGTCCCAGAGCTCAGCCCTGGCCCTCAAGACTTGAAGAAGAGGAGG
 CAGATGAGACTGAGACGGCGTGGCGCCTTGCCGGCTGTCCCCTGCGACTACGACCACGTG
 CGACACCTGCAGGTGCCCTGCAAGGAGCTACAGAGGGTCGGGCCGGCCTGCCTGTGCC
 AGGACTCTCCAGCCCCGCCAGCCGCCCCGACCCGCGCATGGAGAAGTGCACATTGCGG
 CCGAAGAGGGCCGCGCAGTGGTCACTGGTGTGCCCTCTCCCCGGTCCACTACTGG
 CTGCTGCTTGGGACGGCAGCGAGGCTGCCAGAAGGGGCCCCGCTGAACGCTACGGTCCG
 CAGAGCCGAACTGAAGGGGCTGAAGCCAGGGGCATTATGTCGTTGCGTAGTGGCCGCTA
 ACGAGGCCGGGCAAGCCGCGTCCCCAGGCTGGAGGAGAGGGCCTCGAGGGGCCGACATC
 CCTGCCTTCGGGCCTTGAGCCGCTTGCGGTGCCGCCAACCCCCGCACTCTGGTCCACGC
 GGCGTCGGGTGGCACGGCCCTGGCCCTGCTAACGCTGTGCCGCCCTGGTGTGGCACTTCT
 GCCTGCACGATCGCTGGGCTGCCCGAGCCGCCGAGCCGAGGGCGCT**TGA**
 AAGGGGCCTGGGGCATCTCGGGCACAGACAGCCCCACCTGGGCGCTCAGCCTGGCCCCG
 GGAAAGAGGAAAACCGCTGCCTCCAGGGAGGGCTGGACGGCGAGCTGGAGCCAGCCCCAG
 GCTCCAGGGCCACGGCGAGTCATGGTCTCAGGACTGAGCGCTTGTAGGTCCGGTACTT
 GGCGCTTGTTCCTGGCTGAGGTCTGGGAAGGAATAGAAAGGGGCCCAATTTTTTA
 AGCGGCCAGATAATAATAATGTAACCTTGCAGGTTAAAAAAAAAAAAAAA

FIGURE 152

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68874
><subunit 1 of 1, 238 aa, 1 stop
><MW: 25262, pI: 6.44, NX(S/T): 1
MLGSPCLLWLLAVTFLVPRAQPLAPQDFEEEADETETAWPPLPAVPCDYDHCRHLQVPCKE
LQRVGPAAACLCPGLSSPAQPPDPPRMGEVRIAAEEGRAVVHWCAPFSPVLHYWLLLWDGSEA
AQKGPPPLNATVRRaelKGLKPGGIYVVCVVAANEAGASRVPQAGGELEGADIPAFGPCSRL
AVPPNPRTLVHAAVGVGTALALLSCAALVWHFCLDRWGCPAAAARAAGAL
```

Important features of the protein:

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 194-220

N-glycosylation site.

amino acids 132-135

FIGURE 153

AGAGAAAGAAGCGTCTCCAGCTGAAGCCAATGCAGCCCTCCGGCTCTCCGCGAAGAAGTTCC
 CTGCCCGATGAGCCCCCGCCGTGCGTCCCCGACTATCCCCAGGCAGGGCGTGGGCACCGGG
 CCCAGCGCCGACGATCGTGCCTTGCCTGGGAGTAGGATGTGGTGAAAGGATGGGC
 TTCTCCCTTACGGGGCTACA**ATG**GCCAGAGAAGATTCCGTGAAGTGTCTGCCTGCCTGCT
 CTACGCCCTCAATCTGCTCTTTGGTTAATGTCCATCAGTGTGGCAGTTCTGCTTGGA
 TGAGGGACTACCTAAATAATGTTCTCACTTAACAGCAGGGTAGAGGAAGCAGTC
 ATTTGACTTACTTCTGTGGTCATCCGGTATGATTGCTGTTGCTGTTCTGCATGGTACT
 TGTGGGGATGTTAGGATATTGTGGAACGGTGAAAAGAAAATCTGTTGCTTCTGCATGGTACT
 TTGGAAGTTGCTTGTGTTAGAAGTGGCTTGCGTTGGACATATGAACAG
 GAACTATGGTCCAGTACAATGGTCAGATATGGTCACTTGAAGGCCAGGATGACAAATTA
 TGGATTACCTAGATATCGGTGGCTACTCATGCTTGAATTTCAGAGAGAGTTAAGT
 GCTGTGGAGTAGTATATTCACTGACTGGTGGAAATGACAGAGATGGACTGGCCCCAGAT
 TCCTGCTGTGTTAGAGAATTCCCAGGATGTTCAAACAGGCCACCAGGAAGATCTCAGTGA
 CCTTTATCAAGAGGGTTGTGGGAAGAAAATGTATTCTTTGAGAGGAACCAAACACTGC
 AGGTGCTGAGGTTCTGGGAATCTCCATTGGGTGACACAAATCCTGGCATGATTCTCACC
 ATTACTCTGCTCTGGCTCTGTATTATGATAGAACAGGAGCCTGGACAGACAAATGATGTC
 CTTGAAGAATGACAACACTCAGCACCTGTATGTCCTCAGTAGAACTGTTGAAACCAAGCC
 TGTCAAGAATCTTGAACACACATCCATGGCAAACAGCTTAAATACACACTTGAGATGGAG
 GAGTT**TAA**AAAGAAATGTCACAGAAGAAAACCACAAACTGTTTATTGGACTTGTGAATT
 TTTGAGTACATACATATGTGTTCAGAAATATGTAGAAATAAAATGTGCCATAAAATAACA
 CCTAAGCATATACTATTCTATGCTTAAATGAGGATGGAAAAGTTCATGTCATAAGTCAC
 CACCTGGACAATAATTGATGCCCTTAAATGCTGAAGACAGATGTACATACCCACTGTGTAGC
 CTGTGTATGACTTTACTGAACACAGTTATGTTGAGGCAGCATGGTTGATTAGCATTTC
 CGCATCCATGCAAACGAGTCACATATGGTGGACTGGAGCCATAGTAAAGGGTGTATTACTT
 CTACCAACTAGTATATAAGTACTAATTAAATGCTAACATAGGAAGTTAGAAAATACTAATA
 ACTTTATTACTCAGCGATCTATTCTCTGATGCTAAATAATTATATCAGAAAACCTTC
 AATATTGGTGAACACATTGTCTTAAGCTGATCAGGGATTTGTATATAAGTCTGTGTTAAA
 GAGCAAGCTAACACATTGTCTTAAGCTGATCAGGGATTTGTATATAAGTCTGTGTTAAA
 TCTGTATAATTCACTGATTCAGTTCTGATAATGTTAAGAATAACCATTATGAAAAGGAAA
 ATTTGCTCTGTATAGCATCATTATTTAGCCTTCTGTTAATAAAAGCTTACTATTCTGT
 CCTGGGCTTATATTACACATATAACTGTTATTTAAATCTAACCACTAATTGAAAATTA
 CCAGTGTGATACATAGGAATCATTATTCAAGAATGTAGTCTGGTCTTAGGAAGTTAAATA
 GAAAATTGCACATAACTTAGTTGATTCAAGAAGGACTTGTATGCTGTTCTCCAAATG
 AAGACTCTTTGACACTAAACACTTTAAAAAGCTTATCTTGCCCTCTCCAAACAAGAA
 GCAATAGTCTCCAAGTCATATAAAATTCTACAGAAAATAGTGTCTTTCTCAGAAAAT
 GCTTGTGAGAATCATTAAACATGTGACAATTAGAGATTCTTGTGTTATTCACTGATTA
 ATATACTGTGGCAAATTACACAGATTAAATTGTTACAAGAGTATAGTATATTGAA
 GAAATGGAAAAGTGCATTACTGTTGTTGTTATTCAGAATATGGAA
 AGAAAATTAAATGTGTCAATAATATTCTAGAGAGTAA

FIGURE 154

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68880
><subunit 1 of 1, 305 aa, 1 stop
><MW: 35383, pI: 5.99, NX(S/T): 0
MAREDSVKCLRCLLYALNLLFWLMSISVLAWSAWMRDYLNNVLTLTAETRVEEAVILTYFPV
VHPVMIAVCCFLIIVGMLGYCGTVKRNLNLAWYFGSLLVIFCVELACGVWTYEQELMVPVQ
WSDMVTLKARMTNYGLPRYRWLTHAWNFFQREFKCCGVYYFTDWLEMTEMDWPPDSCCVREF
PGCSKQAHQEDLSDLYQEGCGKKMYSFLRGTKQLQVLRFGLGISIGVTQILAMILTTLLWAL
YYDRREPDTDQMMSLKNDNSQHLSCPSVELLKPSLSRIFEHTSMANSFNTHFEMEEL
```

Signal peptide:

amino acids 1-33

Transmembrane domains:

amino acids 12-35, 57-86, 94-114, 226-248

FIGURE 155

GAGAGAGGCAGCAGCTGCTCAGCGACAAGGATGCTGGCGTGAGGGACCAAGGCCTGCC
 TGCACTCGGGCCTCCTCCAGCCAGTGCTGACCAGGGACTTCTGACCTGCTGGCCAGCCAGGA
 CCTGTGTGGGAGGCCCTCCTGCTGCCTGGGTGACAATCTCAGCTCCAGGCTACAGGGAG
 ACCGGGAGGATCACAGAGCCAGC**ATG**TACAGGATCCTGACAGTGATCAACCTCTGAACAGC
 CTCGATGTCAAACCCCTGCGCAAACCCGTATCCCCATGGAGACCTCAGAAAGGTGGGAT
 CCCCATCATCATAGCACTACTGAGCCTGGCGAGTATCATCATTGTGGTTGCCTCATCAAGG
 TGATTCTGGATAAATACTACTTCCTCTGCGGGCAGCCTCTCCACTTCATCCGAGGAAGCAG
 CTGTGTGACGGAGAGCTGGACTGTCCCTGGGGAGGACGAGGAGCAGTGTCAAGAGCTT
 CCCCAGGGCCTGCAGTGGCAGTCCGCCTCTCCAAGGACCGATCCACACTGCAGGTGCTGG
 4 ACTCGGCCACAGGAACTGGTTCTCTGCCTGTTGACAACCTCACAGAACGCTCTCGCTGAG
 0 ACAGCCTGTAGGCAGATGGGCTACAGCAGAGCTGTGGAGATTGGCCAGACCAGGATCTGGA
 3 TTGTTGAAATCACAGAAAACAGCCAGGAGCTCGCATCGGAACACTCAAGTGGCCCTGTC
 7 TCTCAGGCTCCCTGGCTCCCTGCACTGTCTGCCTGTGGAAAGAGCCTGAAGACCCCCGT
 6 GTGGTGGGTGGGGAGGAGGCCTCTGTGGATTCTTGGCCTGGCAGGTCAGCATCCAGTACGA
 9 CAAACAGCACGTCTGTGGAGGGAGCATTGGACCCCCACTGGTCCTCACGGCAGCCCAC
 2 GCTTCAGGAAACATACCGATGTGTTCACTGGAAGGTGCGGGCAGGCTCAGACAAACTGGC
 4 AGCTTCCCACCCCTGGCTGTGGCCAAGATCATCATCATTGAATTCAACCCATGTACCCAA
 7 AGACAATGACATGCCCTCATGAAGCTGCAGTCCACTCACTTCTCAGGCACAGTCAGGC
 4 CCATCTGTCTGCCCTTTGATGAGGAGCTCACTCCAGCCACCCACTCTGGATCATTGGA
 TGGGGCTTACGAAGCAGAATGGAGGGAAAGATGTCTGACATACTGCTGCAGGCGTCAGTCCA
 GGTCAATTGACAGCACACGGTCAATGCAGACGATGCGTACCGAGGGAAAGTCACCGAGAAGA
 TGATGTGTGCAGGCATCCCGAAGGGGGTGTGGACACCTGCCAGGGTACAGTGGTGGGCC
 CTGATGTACCAATCTGACCAGTGGCATGTGGTGGCATCGTAGCTGGGCTATGGCTGCC
 GGGCCCGAGCACCCCCAGGAGTATACACCAAGGTCTCAGCCTATCTCAACTGGATCTACAATG
 TCTGGAAGGCTGAGCTG**TAA**TGCTGCTGCCCTTGCACTGCTGGAGGCCGCTCCTCCTG
 CCCTGCCACCTGGGATCCCCAAAGTCAGACACAGAGCAAGAGTCCCCTGGGTACACCC
 CTCTGCCACAGCCTCAGCATTCTGGAGCAGCAAAGGGCCTCAATTCTGTAAGAGACCC
 TCGCAGCCCAGAGGCGCCAGAGGAAGTCAGCAGCCCTAGCTCGGCCACACTGGTGCTCCC
 AGCATCCCAGGGAGAGACACAGCCCAGTGAACAAGGTCTCAGGGTATTGCTAAGCCAAGAA
 GGAACCTTCCCACACTACTGAATGGAAGCAGGCTGTCTGTAAAAGCCCAGATCACTGTGGG
 CTGGAGAGGAGAAGGAAAGGGTCTGCCAGCCCTGCCGTCTCACCCATCCCCAAGCCTA
 CTAGAGCAAGAACCAAGTGTAAATATAAAATGCACTGCCCTACTGTTGGTATGACTACCGTT
 ACCTACTGTTGTCAATTGTTATTACAGCTATGCCACTATTATTAAAGAGCTGTGTAACATCT
 CTGGCAAAAAAA

FIGURE 156

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA68885
><subunit 1 of 1, 432 aa, 1 stop
><MW: 47644, pI: 5.18, NX(S/T): 2
MLQDPDSDQPLNSLDVKPLRKPRIPMETFRKVGIPIIALLSLASIIIVVVLIKVILDKYF
LCGQPLHFIPRKQLCDGELDCPLGEDEEHCVKSFPPEGPAVAVRLSKDRSTLQVLDSATGNWF
SACFDNFTEALAETACRQMGYSRAVEIGPDQDLDVVEITENSQELMRNRSSGPCLSGSLVSL
HCLACGKSLKTPRVVGEEASVDSWPWQVSIQYDKQHVCGGSILDPHWVLTAACFRKHTDV
FNWKVRAGSDKLGSFPSLAVAKIIIIEFNPMPKDNDIALMKLQFPLTFSGTVRPICLPFFD
EELTPATPLWIIGWGFTKQNGGKMSDILLQASVQVIDSTRCNADDAYQGEVTEKMMCAGIPE
GGVDTQCQGDSGGPLMYQSDQWHVVGIVSWGCGGPSTPGVYTKVSAYLNWIYNVWKAEL
```

Transmembrane domain:

amino acids 32-53 (typeII)

FIGURE 157

GGGCTGAGGCAGTGAGAGACCGGAAAGCCTGGCATTCCAGAGGGAGGGAAACGCAGCGCATCCCCAGGCTCCAG
 AGCTCCCTGGTGACAGTCTGGCTGAGCATGGCCCTCCAGCCCTGGCCTGGAGCCCTGGAGCCTCTGGGCC
 TTTTCCTCTTCAACTGCTCAGCTGCTGCCAGCACGCCGGGGAGGCCAGGGCCATGCCA
 GGGTCAGATACTATGCAGGGATGAACGTAGGGCACTTAGCTTCCACCAGAACGGCCTCCAGGATTTGACA
 CTCTGCTCCTGAGTGGTATGAAATACTCTACGTGGGGCTGAGAACGCCATTCTGGCTTGGATATCCAGG
 ATCCAGGGTCCCCAGGCTAAAGAACATGATAACCGTGGCCAGCCAGTGACAGAAAAAGAGTGAATGTGCCTTA
 AGAAGAACAGCAATGAGACACAGTGTTCAACTTCATCCGTGCTGGTTCTACAATGTCACCCATCTACAA
 CCTGGGGCACCTCGCCCTCAGCCCTGCTTACCTTCATTGAACCTCAAGATTCCACCTGTTGCCCATCTCGG
 AGGACAAGGTATGGAGGGAAAAGGCCAAAGCCCCTTGACCCGCTCACAAGCATAAGGCTGTCTGGTGGATG
 GGATGCTCTATTCTGGTACTATGAACAACCTCCTGGCAGTGAGCCATCCTGATGCGCACACTGGATCCCAGC
 CTGTCCTCAAGACCGACAACCTCCTCCGCTGGCTGCATCATGACGCCCTCTTGTGGCAGGCCATCCCTCGACCC
 H AGGTGCTCTACTTCTTCTCGAGGAGACAGCCAGCGAGTTGACTTCTTGAGAGGGCTCCACACATCGGGGTGG
 CTAGAGTCTGCAAGAACATGACGTGGCGCGAAAAGCTGCTGCAGAACAGTGGACCACCTTCTGAAGGCCAGC
 TGCTCTGCACCCAGCCGGGGCAGCTGCCCTCAACGTCATCCGCCACGCCGCTGCTCCCCGCCGATTCTCCA
 CAGCTCCCCACATCTACGCACTTCACCTCCCAGTGGCAGGTTGGCGGGACCAGGAGCTGCGGTTGTGCT
 TCTCTCTTGGACATTGAACGTGTTAAGGGAAATACAAAGAGTGAACAAAGAAACTTCACGCTGGACTA
 CTTATAGGGCCCTGAGACCAACCCCGCCAGGCAGTTGCTCAGTGGCCCTCCTCTGATAAGGCCCTGACCT
 TCATGAAGGACCATTCTGATGGATGAGCAAGTGGTGGGACGCCCTGCTGGTAAATCTGGCTGGAGTATA
 CACGGCTGCACTGGAGACAGCCAGGGCCTTGATGGGACAGCCATCTTGTATGTAACCTGGGAAACCACACAG
 GGTGCTCCACAAGGCTGTTAAGTGGGACAGCAGTGCTCATCTGGTGAAGAGATTGAGCTGTTCCCTGACC
 CTGAACCTGTTGCAACCTGCACTGGCCCCACCCAGGGTGCAGTGGTAGGCTCTCAGGAGGTGTCTGGA
 GGGTGCCTGGAGCAACTGTAGTGTCTATGAGAGCTGTGACTGTGCTTGGCCGGGACCCCCACTGTGCCT
 GGGACCCCTGAGTCCGAACCTGTTGCCCTCTGTCGCCCTAACCTGAACCTGGAAAGCAGGACATGGAGCGGG
 GGAACCCAGAGTGGCATGTGCCAGTGGCCCTGAGCAGGAGCCCTGCCCTCAGAGCCGCCCAAATCATTA
 AAGAACGTCTGGCTGCCCCAACTCCATCCTGGAGCTCCCTGCCCTGCCCCACTGTCAACCTGGCTTATTATT
 GGAGTCATGGCCAGCAGCAGTCCCAGAACGCTCTTCACTGTCTACAATGGCTCCCTTGCTGATAGTGCAGG
 ATGGAGTTGGGGCTCTACCAGTGCTGGCAACTGAGAACATGGTTTCAACCTGTGATCTCTACTGGGTGG
 ACAGCCAGGACCAGCCCTGGCCCTGGATCTGAACGGCATCCCCGGGAGCATGTGAAGGTCCCGTTGA
 CCAGGGTCAGTGGTGGGCCGCCCTGGCTGCCAGCAGTCTACTGGCCCACTTGTCACTGTACTGTCT
 TTGCTTAGTGCTTCAAGGAGCCCTCATCATCCTCGTGGCTGCCCTGGGACTTGTGAGAGCACTCCGGCTCGGGCAAGG
 TTCAGGGCTGTGAGACCCCTGCCCTGGGAGAACGGCCCTGTTAAGCAGAGAGCAACACCTCCAGTCTCCAAAGG
 AATGCAGGACCTGCCAGTGATGTGGACGCTGACAACAACTGCCCTAGGCACTGAGGTAGCTTAAACTCTAGGCA
 CAGGCCGGGCTGCCGTGAGGACGCCAGTGGCTGGCTGGCCCAAGCACAGCCCTGACTAGGATGACAG
 CAGCACAAAAGACCACTTCTCCCTGAGAGGAGCTCTGCTACTCTGCATCACTGATGACACTCAGCAGGGTG
 ATGCACAGCAGTCTGCCCTCCCTATGGACTCCCTTCACTAACGACATGAGCTCTCAACAGGGTGGGGCTAC
 CCCCCAGACCTGCTCTACACTGATATTGAAGAACCTGGAGAGGATCCTCAGTCTGCCATTCCAGGGACCCCTC
 CAGAAACACAGTGGTCAAGAGACCTAAAAACCTGCCCTGGAAACTCCACTCTGAAGCTGCCGCTTGGACACCAACACTCC
 TAAACAATCATATGCTAACATGCCACTGCCAGTGGAAACTCCACTCTGAAGCTGCCGCTTGGACACCAACACTCC
 TCTCCCAAGGGTATGCCAGGGATCTGCTCCCTGCCCTGCTTACCTAGCTGCCCTGACTCCAGGAAGTC
 TTTCCCTGAAGTCTGACCACTTCTTCTGCTTACCTAGCTGCCCTGACTCCAGGAAGTC
 CAGGGGTAATCTGAGCCTTCTCACTCCTTACCTAGCTGCCCTGACTCCAGGAAGTC
 TTTGGGATTCAAGAAAATGCTTGTCAAGAGACTGTTATTAAAAATATAAGGCTTAAAAAAA

FIGURE 158

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71166
><subunit 1 of 1, 761 aa, 1 stop
><MW: 83574, pI: 6.78, NX(S/T): 4
MALPALGLDPWSLLGLFLQQLQLLLPTTAGGGGQGPMPVRYYAGDERRALSFFHQKGLQ
DFDTLSSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAFKKKSNETQC
FNFIRVLVSYNVTHLYTCGTFAFSPACTFIELQDSYLLPISEDKVMEGKGQSPFDPAHKHTA
VLVDGMLYSGMTMNNFLGSEPILEMRILGSQPVLKTDNFLRWLHHDASFVAAIPSTQVVYFFF
ETASEFDFFERLHTSRVARVCKNDVGEKLLQKKWTTFLKAQLLCTQPGQLPFNVIRHAVLL
PADSPTAPIYAVFTSQWQVGGTRSSAVCAFSLLDIERVFKGKYKELNKETSRWTTYRGPET
NPRPGSCSVGPSSDKALTFMKDHFMLDEQVVGTPLLVKSGVEYTRLAVETAQGLDGHSHLVM
YLGTTTGSLLHKAVVSGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGVWRVPRAN
CSVYESCVDCVIARDPHCAWDPEPESRTCCLLSAPNLNSWKQDMERGNPEWACASGPMSRSLRP
QSRPQIIKEVLAVPNISILELPCPHLSALASYWSHGPAAVPEASSTVYNGSLLLIVQDGVGG
LYQCWATENGFSYPVISYWVDSQDQLALDPELAGIPREHVKVPLTRVSGGAALAAQQSYWP
HFVTVTVLFALVLSGALIILVASPLRALRARGKVQGCETLRPGEKAPLSREQHLQSPKECRT
SASDVADNNCLGTEVA
```

Signal peptide:

amino acids 1-30

Transmembrane domains:

amino acids 136-156, 222-247, 474-490, 685-704

FIGURE 159

AGGGTCCCTAGCCGGCGCAGGGCGCGCAGCCCAGGCTGAGATCCGGCTTCCGTAGAAG
 TGAGC**ATG**GCTGGGCAGCGAGTCTTCTAGTGGCTTCCTCTCCCTGGGGCTGCTC
 TCAGAGGCTGCCAAAATCCTGACAATATCTACAGTAGGTGGAAGCCATTATCTACTGATGGA
 CCGGGTTTCTCAGATTCTCAAGATCACGGTCATAATGTCACCATGCTAACCAAAAGAG
 GTCCTTTATGCCAGATTTAAAAGGAAGAAAATCATATCAAGTTATCAGTTGGCTTGCA
 CCTGAAGATCATCAAAGAGAATTAAAAAGAGTTGATTTCTTCTGGAAAGAAACTTTAGG
 TGGCAGAGGAAAATTGAAAATCTTAAATGTTCTAGAATACTTGGCGTTGCAGTGCAGTC
 ATTTTTAAATAGAAAGGATATCATGGATTCTAAAGAATGAGAACATCGACATGGTGATA
 GTTGAACACTTTGACTACTGTCCTTCTGATTGCTGAGAACGCTGGGAAGCCATTGTC
 CATTCTTCCACTTCATTGGCTCTTGGAAATTGGGCTACCAATCCCCCTGCTTATGTC
 CAGTATTCCGTTCTGCTGACTGATCACATGGACTCTGGGGCCGAGTGAAGAATTCTG
 ATGTTCTTAGTTCTGCAGGAGGCAACAGCACATGCACTACATTGACAACACCATCAA
 GGAACATTTCACAGAAGGCTTAGGCCAGTTGCTCATCTACTGAAAGCAGAGTTGT
 GGTCATTAACTCTGACTTGCCTTGATTTGCTCGACCTCTGCTTCCAACACTGTTAT
 GTTGGAGGCTTGATGAAAAACCTATTAAACCACTGACCTGGAGAACATTGTCATTG
 CAAGTTGGGACTCTGGTTTGTGACCTGGCTCCATGGTAACACCTGTCAGA
 ATCCGAAATCTCAAGGAGATGAACAATGCCTTGCTCACCTACCCAAGGGGTGATATGG
 AAGTGTCACTGTTCTCATTGCCAAAGATGTCCACCTGGCTGCAAATGTGAAAATTG
 CTGGCTCCTCAGAGTGCACCTGGCTCACCAAGCATCCGCTGTTGTACCCACGGCG
 GGCAGAATAGCATAATGGAGGCCATCCAGCATGGTGTGCCATGGTGGGATCCCTCTT
 GGAGACCAGCCTGAAAACATGGTCCGAGTAGAACGCAAAAGTTGGTGTCTATTCA
 AAAGAAGCTCAAGGAGACATTGGCTCTAACATGAAACAAATCATGGAAGACAAGAGAT
 ACAAGTCCGGCAGTGGCTGCCAGTGTACCTGCGCTCCACCGCTCAGCCCCACACAG
 CGGCTGGTGGGCTGGATTGACCACGTCTCCAGACAGGGGGCGCAGCACCTCAAGCC
 TGTCTTCAGCAGCCCTGGCATGAGCAGTACCTGTCGACGTTTGTGTTCTGCTGGG
 TCACTCTGGGACTCTATGGCTTGAGCTGCTGGCATGGCTGTCTGGTGGCTGCGT
 GGGGCCAGAAAGGTGAAGGAGACAT**TAA**GGCCAGGTGCAGCCTGGCAGGGCTGTTGG
 GCGATGTCACCATTCTAGGGAGCTTCCACTAGTTCTGGCAGCCCCATTCTCTAGTC
 TAGTTATCTCTGTTTCTGAAGAACAGGAAAAATGCCAAAATCATCCTTCACTG
 TAATTTGCTACAAATTCTACTAGCTCCTGCCTGCTAGCAGAAATCTTCCAGTCT
 CTTGTCCTCCTTGTGCTGCCATCAGCAAGGGCTATGCTGTGATTCTGCTCTGAGT
 GACTTG
 GACCACTGACCCCTCAGATTCCAGCCTAAAATCCACCTCCTCTCATGCGCTCTCGAA
 TCACACCCCTGACTCTCCAGCCTCCATGTCAGACCTAGTCAGCCTCTCACTCCTGCC
 TACTATCTATCATGGAATAACATCCAAGAAAGACACCTTGCAATTCTTCA
 TGTTCTCCCACATATTCTTCAATGCTCAGGAAGCCTGCCCTGTGCTTGAGAGTT
 CGGACACAGGCTCACAGGTCTCCACATTGGGTCCTGTCTGGTGCCCACAGTGAG
 CCTCTGGCTGAGCAGGCATGGAGACTGTAGGTTCCAGATTCTGAA
 AAAAATAAAGTTACA
 GCGTTATCTCTCCCCAACCTCACTAA

FIGURE 160

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71169
><subunit 1 of 1, 523 aa, 1 stop
><MW: 59581, pI: 8.68, NX(S/T): 1
MAGQRVLLVGFLPGVLLSEAAKILTISTVGGSHYLLMDRVSQILQDHGHNVMTMLNHKRGP
FMPDFKKEEKSYQVISWLAPEDHQREFKKSFDFFFLEETLGGRGKFENLLNVLEYLALQCSHF
LNRKDIDMSLKNENFDMVIVETFDYCPFLIAEKLGKPFVAILSTSGSLEFGLPIPLSYVPV
FRSLLTDHMDFWGRVKNFLMFFSFCRRQQHMQSTFDNTIKEHFTEGSRPVLSHLLLKAELWF
INSDFAFDFARPLLPNTVYVGGLMEKPIKPVPQDLENFIAKFGDSGFVLVTLGSMVNTCQNP
EIFKEMNNNAFAHLPQGVIWKCQCQSHWPKDVKLAANVKIVDWLPQSDLAAHPSIRLFVTHGGQ
NSIMEAIQHGVPVMVGIPLFQGDQOPENMVRVEAKKFGVSIQLKKLKAETLALKMKQIMEDKRYK
SAAVAASVILRSHPLSPTQRLVGWIDHVLQTGGATHLKPYVFQQPWHEQYLFDVFVFLGLT
LGTLWLCGKLLGMAVWWLRGARKVKET

Topomer = 69351003 T

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 483-504

FIGURE 161

GGGCTGTTGATTGTGGGGGATTTGAAGAGAGGGAGGAATAGGAGGAAGGGGTTGAGGGGCT
 GCCTCTGGCATATGCACACACTCACACATTCTGTACACCCGTACACACACATACCATGTT
 CTCCATCCCCCAGGTCCAGGCCCTCAGTGCTGTCCCACCCAGCAGGGCTACCTGAAGCTCT
 GGCTGCAGCCCTCCCGTCCAGTGGCAGGGCGCTTCATCCCTCCTTCTCTCCAAAGCCCA
 ACTGCTGTCAGTGCATGCTTGCCAAGGAGGGAACTGCAGTGACAGCAGGAGTAAGAGT
 GGGAGGCAGGACAGAGCTGGGACACAGGTATGGAGAGGGGTTCAGCGAGCCTAGAGAGGGC
 AGACTATCAGGGTGCCGGCGGTGAGAATCCAGGGAGAGGAGCGGAAACAGAACAGAGGGGCAGA
 AGACCGGGGCACTTGTGGGTTGCAGAGCCCTCAGCC**ATGT**TGGGAGCCAAGCCACACTGGC
 TACCAGGTCCCTACACAGTCCGGCTGCCCTGGTTCTGGTGCCTCTGGCCTGGGGGCC
 GGGTGGGCCAGGAGGGTCAGAGCCGTCCTGCTGGAGGGGAGTGCCTGGTGGTCTGTGA
 GCCTGGCCGAGCTGCTGCAGGGGGCCGGGGAGCAGCCCTGGGAGAGGCACCCCTGGC
 GAGTGGCATTGCTGCGGTCCGAAGCCACCATGAGCCAGCAGGGAAACCGGCAATGGC
 ACCAGTGGGCCATCTACTTCGACCAGGTCTGGTGAACGAGGGCGTGGCTTGACGGGC
 CTCTGGCTCCTCGTAGCCCTGTCCGGGGTGTCTACAGCTCCGGTCCATGTGGTGAAGG
 TGTACAACCGCAAACGTGTCAGGTGAGCCTGATGCTGAACACGTGGCCTGTCTCAGCC
 TTTGCCAATGATCCTGACGTGACCCGGGAGGCAGCCACCATGAGCTCTGTGCTACTGCCCTTGA
 CCCTGGGGACCGAGTGTCTCTGCCCTGCGTCGGGGAAACTACTGGGTGGTGGAAATACT
 CAAGTTCTCTGGCTTCATCTTCCCTCT**TGA**GGACCAAGTCTTCAAGCACAAGAAT
 CCAGCCCTGACAACCTTCTTCTGCCCTCTGGCCAGAAAACAGCAGAGGCAGGAGAGAG
 ACTCCCTCTGGCTCCTATCCCACCTCTTGATGGGACCCCTGTGCCAAACACCCAAAGTTAA
 GAGAAGAGTAGAGCTGTGGCATCTCCAGACCAGGCCTTCCACCCACCCACCCAGTTACC
 CTCCCAGCCACCTGCTGCATCTGGCTCTGCCCTGCAGCCCTAGGATCAGGGCAAGGTTGGCA
 AGAAGGAAGATCTGCACTACTTGCGGCCTGTCTCCGGTCCCCACCCAGCTTCC
 GCTCAATGCTGATCAGGGACAGGTGGCGCAGGTGAGCCTGACAGGCCACAGGAGCCCAG
 ATGGACAAGCCTCAGCGTACCCCTGCAGGCTTCTCCTGTGAGGAAGCCAGCATCACGGATC
 TCAGCCAGCACCGTCAGAAGCTGAGCCAGCACCGTATGGCTAGGGTGGGAGGCTAGCCAC
 AGGCAGAAGGGTGGGAAGGGCTGGAGTCGTGGCTGGTGGAGGAAGGAAGGAGGGTGTATTG
 TCTAGACTGAACATGGTACACATTCTGCATGTATAGCAGAGCAGCCAGCAGGTAGCAATCCT
 GGCTGTCCTTCTATGCTGGATCCCAGATGGACTCTGGCCCTTACCTCCCCACCTGAGATTAG
 GGTGAGTGTGTTGCTCTGGCTGAGAGCAGAGCTGAGAGCAGGTATACAGAGCTGGAAGTGG
 ACCATGGAAAACATCGATAACCATGCACTCTTGCTTGGCCACCTCCTGAAACTGCTCCAC
 CTTTGAAGTTGAACCTTACTGCTCCACACTCTGACTGCTGCCTCCTCCTCCAGCTCTC
 TCACTGAGTTATCTTCACTGTACCTGTTCCAGCATATCCCCACTATCTCTCTTCTGAT
 CTGTGCTGTCTTATTCTCCTCTAGGCTCCTATTACCTGGATTCCATGATTCAATTCTT
 CAGACCCCTCTCCGCCAGTATGCTAAACCTCCCTCTCTTCTTATCCGCTGTCCATT
 GGCCAGCCTGGATGAATCTATCAATAAAACAATAGAGAATGGTGGTCAGTGAGACACTAT
 AGAATTACTAAGGAGAAGATGCCCTGGAGTTGGATGGGTGTTACAGGTACAAGTAGGTA
 TGTTGCAGAGGAAAATAATCAAACGTATGATACTAAAATTAAAAA

FIGURE 162

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71180
><subunit 1 of 1, 205 aa, 1 stop
><MW: 21521, pI: 7.07, NX(S/T): 1
MLGAKPHWLPGPLHSPGPLPLVLLALGAGWAQEGSEPVILLEGECLVVCEPGRAAAGGPGGA
ALGEAPPGRVAFAAVRSHHHEPAGETGNGTSGAIYFDQVLVNEGGGFDRASGSFVAPVRGVY
SFRFHVVVKVYNRQTQVQVSLMLNTWPVISAFAFPDVTRREAATSSVLLPLDPGDRVSLRLRRG
NLLGGWKYSSFSGFLIFPL
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Signal peptide:

amino acids 1-32

FIGURE 163

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GCTGTTCTCTCGGCCACCACTGGCCGGCGCAGCTCCAGGTGTCCTAGCCGCCAGC
 CTCGACGCCGTCCCAGGGACCCCTGTGCTCTGCAGAAGCCCTGGCCCCGGGGCCGGGCAT
 GGGCCAGGGCGCGGGGTGAAGCGGCTTCCCGCGGGCGTGACTGGGCGGGCTTCAGCC**AT**
GAAGACCCTCATAGCCGCCTACTCCGGGTCCTGCAGCGAGCGTCAGGCCGAGGCTGACC
 GGAGCCAGCGCTCTCACGGAGGACCTGCCTGCGCGAGGGCTGGGAGATGGGCAGT
 GGATCCAGCATCCTCTCCGCCCTCCAGGACCTCTCTGTACCTGGCTAACAGGTCAA
 GGTGGAAAAGCAGCTACAGGTATCTCAGTGCTCCAGTGGCCTGTCCTCCTGTACTGG
 GAGTGGCCTGCAGTGCCATCCTCATGTACATATTCTGACTGATTGCTGGCTCATCGCTGTG
 CTCTACTTCACTTGGCTGGTGTGTTGACTGGAACACACCCAAGAAAGGTGGCAGGAGGTACA
 GTGGGTCGAAACTGGGCTGTGGCGCTACTTCGAGACTACTTCCATCCAGCTGGTGA
 AGACACACAACCTGCTGACCACCAGGAACATATATCTTGGATACCACCCCCATGGTATCATG
 GGCCTGGGTGCCTCTGCAACTTCAGCACAGAGGCCACAGAAGTGAGCAAGAAGTTCCCAGG
 CATAACGGCCTTACCTGGCTACACTGGCAGGCAACTCCGAATGCCTGTGTTGAGGGAGTACC
 TGATGTCTGGAGGTATCTGCCCTGTCAGCCGGACACCATAAGACTATTGCTTCAAAGAAT
 GGGAGTGGCAATGCTATCATCATCGTGGTCGGGGTGCAGCTGAGTCTCTGAGCTCCATGCC
 TGGCAAGAATGCAGTCACCCCTGCGGAACCGCAAGGGCTTGTGAAACTGGCCCTGCGTCATG
 GAGCTGACCTGGTCCCCTACTCCTTGGAGAGAAATGAAGTGTACAAGCAGGTGATCTC
 GAGGAGGGCTCCTGGGGCGATGGTCCAGAAGAAGTTCCAGAAATACATTGGTTCGCCCC
 ATGCATCTTCCATGGTCAGGCCTTCTCCTCCGACACCTGGGGCTGGTGCCTACTCCA
 AGCCCATCACCACTGTTGAGAGCCCACCATCCCCAAGCTGGAGCACCCAAACCCAG
 CAAGACATCGACCTGTACCACACCATGTACATGGAGGCCCTGGTAAGCTTCGACAAGCA
 CAAGACCAAGTCGGCTCCGGAGACTGAGGTCTGGAGGTGAAC**TGA**GCCAGCCTCGGG
 GCCAATTCCCTGGAGGAACCAGCTGCAAATCACTTTTGCTCTGTAAATTGGAAGTGTCA
 TGGGTGTCTGTGGTTATTAAAAGAAATTATAACAATTGCTAAACCAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 164

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71184
><subunit 1 of 1, 388 aa, 1 stop
><MW: 43831, pI: 9.64, NX(S/T): 3
MKTLIAAYSGVLRGERQAEADRSQRSHGGPALSREGSGRWTGSSILSALQDLFSVTWLNR
KVEKQLQVISVLQWVLSFLVLGVACSAILMYIFCTDCWLIAVLYFTWLVDWNTPKKGGRS
QWVRNWAVWRYFRDYFPIQLVKTHNLLTTRNYIFGYHPHGIMGLGAFCNFSTEATEVSKKFP
GIRPYLATLAGNFRMPVLREYLMMSGICPVSRTIDYLLSKNGSGNIIIVVGAAESLSSM
PGKNAVTLRNKRKFVKLALRHGADLVPIYSFGENEVYKQVIFEEGSWGRVQKKFQKYIGFA
PCIFHGRGLFSSDTWGLVPYSKPITTVVGEPITIPKLEHPTQQDIDLYHTMYMEALVKLFDK
HKTGFGLPETEVLEVN
```

Important features of the protein:

Transmembrane domain:

amino acids 76-97

N-glycosylation sites.

amino acids 60-63, 173-176, 228-231

N-myristoylation sites.

amino acids 10-15, 41-46, 84-89, 120-125, 169-174, 229-234, 240-245, 318-323, 378-383

FIGURE 165

GGGGCGGCGGGATGGGGGCCGGGGCGGGCGCCGCACTCGCTAGGGCCCCGACGCAGGGCCGGGCCGGCG
GGGCCGAGGAGCGCGCGGCCAGAGCGGGCGGGAGGCAGCAGCCGGGACGCCCGCGACGAGCAGGTGGCG
GCGGCTCAGGCTTGTCCAGCCGAAGCCCTGAGGGCAGCTGTTCCACTGGCTTGCTGACCTTGTGCCCTGG
CGGCTGTCCTCAGCGAGGGCCGTGCACCGCTCTGAGCAGCGCCATGGGCCTGCTGCCCTCTGAAGACCCA
GTTCGTGTGCACCTGCTGGCTTGTCTCGTGGTAGTGGCTGGCATCAACTCGTCCAGCTGTGCAC
GCTGCGCTCTGCCGGTCAGCAAGCAGCTCACCGCCCTCAACTGCCGCTGCCACTCACTCTGGAGCCA
ACTGGTCATGCTGGAGTGGTGGTCTGCACGGAGTGTACACTGTTACGGGACCAGGCCACGGTAGAGCGCTT
TGGGAAGGAGCACGCAGTCATCATCCTCAACCACAACCTCGAGATCGACTTCCTCTGTGGGTGGACCATGTGTGA
GCGCTCGGAGTGTGGAGCTCCAAGGTCTCGTAAGAAGGAGCTGCTACGTGCCCTCATGGCTGGAC
GTGGTACTTCTGGAGATTGTGTCTGCAAGCGGAAGTGGGAGGAGGCCGGACACCGTGGTCGAAGGGCTGAG
GCGCCTGTCGGACTACCCCGAGTACATGTGGTTCTCTGTACTGCGAGGGGACCGCCTCACGGAGACCAAGCA
CCCGCTTAGCATGGAGGTGGCGCTGTAAGGGCTTCCTGCTCAAGTACCACTGCTGCCCGGACCAAGGG
CTTCACCACCGCAGTCAGTGCTCCGGGGACAGTCGAGCTGTCTATGATGTAACCTGAACCTCAGAGGAAA
CAAGAACCGTCCCTGCTGGGATCCTCTACGGGAAGAAGTACGAGGCGGACATGTGCGTGAGGAGATTTCT
GGAAGACATCCCCTGGATGAAAAGGAAGCAGCTCAGTGGCTTCATAAACTGTACCAAGGAGAAGGACGCGCTCCA
GGAGATATATAATCAGAACGGCATGTTCCAGGGAGCAGTTAACGCTGCCGGAGGCCGTGGACCCCTCTGAA
CTTCCTGTCCTGGGCCACCATTCTCCTGCTCCCTCTCAGTTGTCTGGGCCCTTGCAGCAGGGATCACC
TCTCCTGATCCTGACTTCTGGGTTGTGGAGCAGCTCCTGGAGTTGCAAGACTGATAGGAGAACGCT
TGAACCTGGAGGTGGAGATTGCAGTGAGATGGCATCACTGTAAGTCCAGCCTAGGCAACAGAGCAAGACT
CAGCTCTAAAAAAAAACAAAAACCCCCAGAAATTCTGGAGTGAACCTGTAAGTGGACTGATAGTTACTGACATGAAAA
ATTCACTAGAGGCTAACAGCAGATTGAGCAGGGCAGAAAAATCAGCAAGCTGAAAGATGGTACCTTGAGATT
TTTCAGGCTAATGAAAAAGAATGAAGGAAAATTAAACAGCCTCAGAGACCCATGGTCACCGTCACACAAATCAA
CATATGCATGATGAGAGTCCCAGAACGGAGAGGAGAGAACGGTCAGAAAGAATGCCACAAGCTGATGAAAAACA
GTAACCTACCCACTCAGGAAGCTCAGTGAACCTCAATGAGGATGAATATCAGAGATCCACACCTAGATATTCAT
AATCAAAGTGTCAAATGACAAAGAATCTGAAAGCAGCAAGAGATGAGCAACTTATCTGTTCAAAGGATTTG
ATCAGATTAACAGCTATTCTCCTCAGAAATCATGGGAGCCAGGAGATAGTGGGATGAACACTGTTGAAGGCAA
AACCTCAACTGTAATTATTGGACTTTGAGTCTTAGATGGCCTGACCTTTGTCTTCAGGGACAGTTTCA
ATTTAATCCCTAATAACAATTAGTCAGCTCCTGACCTGTAGGAAGGCTGTCTTAGGCCGGCACAGTGGC
TTACACCTGTAATCCCAGCACTTGGGAGGCCAGACGGGTGGATCATTGGGTCTAGGCTGATCTCAAACCTCT
GAGTCAGGTGATCTGCCCTCAGCTCCAAAGTGTGATTGAGCAGGCTGTAGGACTGCCACTGCCCTGGCGGA
ATTTCTTTAAAGGCTGAATGATGGGGCCAGGCACGATGGCTACGCCGTGATCCAAAGTAGCTTGGATTGTA
AACATGCACCACCATGCCCTGGCTAATTTGTATTTAGTAGAGACGTTAGCCAGGCTGGCTCGATCTCCT
GACCTCAAGTGACCACCTGCCCTAGCCTCCAAAGTACTGGGATTACAGGCGTGAGCCACTGTCCTGGCGTGA
GCATCTTGTGATGTGCTTATTGCCATTGATATCTTCTATCTTCTTGGGAAATGCTGTTCAAGTCCCTTG
CCTTTAAATTTATTATTTATTATTTGAGACAGGGCTTGTGTTGCCAGGCTGGAGTA
CAGTGGCACAGTCTGGCTACTGCAGCCTCGACCTCTGGCTGCAGTGATCCTCCACCTCAGCCTCCCTGT
AGCTGTTTTTTGTATTTGTATTTGTAGCTGTTAGTTGTATTTGTGGAGACAGCATTTCACCATGA
TGCCCAGGCTGGCTTGAACCTCTGAGCTCAAGTGATCTGCCCTGCTTCAGCCTCCAAAGTGTGGGATTACAGA
CATGAGGCCACTGCACCTGGCAAACCTCCAAAATTCAACACACACACACACACACACCTGATCAAAATGGCA
GAGGGGCCGGGTGTGGCCCCAACTACCAGGGAGACTGAAGTGGGAGGATCGCTTGGCATGAGAACGTCAGGCTG
CAGTGAAGTCGAGGTTGTGCGACTGCATTCCAGCCTGGACAACAGAGTGAGACCCCTGTCTC

FIGURE 166

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71213
><subunit 1 of 1, 368 aa, 1 stop
><MW: 42550, pI: 9.11, NX(S/T): 1
MGLLAFLKTQFVLHLLVGFVFVSGLVINFVQLCTLALWPVSKQLYRRLNCRLAYSLWSQLV
MLLEWWSCTECTLFTDQATVERFGKEHAVIILNHNFIEDFLCGWTMCERFGVLGSSKVLAKK
ELLYVPLIGWTWYFLEIVFCKRKWEEDRDTVVEGLRRLSDYPEYMWFLLYCEGTRFTETKHR
VSMEVAAAKGLPVLKYHLLPRTKGFTTAVKCLRGTVAAVYDVTLNFRGNKNPSLLGILYGGKK
YEADMCVRRFPLEDIPLDEKEAAQWLHKLYQEKDALQEIYNQKGMFPGEQFKPARRPWTLLN
FLSWATILLSPLFSFVLGVFASGSPLLILTFLGFVGAASFGVRLIGESLEPGRWRLQ
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 307-323, 335-352

Tyrosine kinase phosphorylation sites.

amino acids 160-168, 161-169

FIGURE 167

GATATTCTTATTTAAGAACCTGAAGTACT**ATG**CATCACTCCCTCCAATGTCCTGGGC
 GCCACCAGGCATATTCATCTTGTGTGTTCTTTGCTTAGCACTGGGCACCTC
 GCTTATTCCTGGTAGGAAAGGGCTCAGTTGTCTGTTGGGTGGCAGGCAGGCC
 GCTTACGCCTGATAACGCCCTGGTTAGAAGGAAGGGAAAGATAAACTTTATACA
 GATAGCTGGGTCTGAGACCTGCTCAGTAAAATTCTGGATCTGCCTATACCTC
 TTCTCTAACCTGGCATACCCCTGCTAAAGCCTCTCAGGCCTCTCTGTTCTAG
 AGTATTAGAGCTACAAGAGCCCTCATGGTCTGGCCCTGCCCTGGCCAGCTCATT
 ACATGTGGTCTTCGTCGTTCTG**TAA**TGTGGTATGCCATGGGTCTTGCACAAGC
 TTCCTCTTGCTGGACACTGTTCCCTGCCCTGGCAGCAGCTGCTACTTAATATG
 ATCCTGCAGATTCAATTCTAACATCATTCTCCAGGGATCCTGGCCTGACAGAATCT
 CTTGTTAATGCTCTCATAAGACCACTGTTCCCTTGAGCACCTGCCACTCAGTG
 TCTTATGTGCGTTGTGGGTATGGGTGTCTGTTCCCCAGAATGCCAGCTTGAG
 TGCGTGAGGGTCAAGGCATTGCTGTGCCAGGTATACTGCCTACATGTGGTGGG
 CATGTTTAGAGACTAAATGGAGGAGGAGATGAGGAAAAGATTGAAATCTCTCAG
 GATGGGTAGGGCCCAGCATTGTAATTACACACGTTGACTGTGCTGTGAATTATC
 TGCAAGGTCTGATTCACTAGGCCAGGTTGGCATCTCTAACAAACTCCCACGTG
 TGCTGGCTATGAACCTAAATAGTAAGAATCTATGGAGCCAGGCTGGCATGG
 TCACACCTATGATCCCAGCACTTGGAGGCTGAGGCAGGCTGATCACCTGGAG
 TCAAGACTAGCCTGGCAAACATGGTGGAACCCATCTGTACTAAAATACACAA
 AACCTGGAGGCGGAGGTTGCAGTGAGCCAGATCAGGCCACTGTATTCCAACC
 AGAGTGGAGACTCTATGTCCAAAAAA
 AAAAAA

FIGURE 168

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71234
><subunit 1 of 1, 143 aa, 1 stop
><MW: 15624, pI: 9.58, NX(S/T): 0
MHHSILQCPGAATRHIHLCVCFSFALALGHFLLISLVGKGLSLSGVGGRQAGLRLIRPWVRR
EGKINFYTNQDSWGLRPASSVKFLGSAYTFFSLTWHTLLKASQGFSLFLGSKYLELQEPEWS
GPPCPPQLHCTCGVLLSFL
```

Important features of the protein:

Signal peptide:

amino acids 1-28

EQUITY INVESTMENT FUND

FIGURE 169

GGCTGGACTGGAACCTCCTGGTCCCAAGTGATCCACCCGCCTCAGCCTCCCAAGGTGCTGTGA
 TTATAGGTGTAAGCCACCGTGTGGCCTCTGAACAACTTTTCAAGCAACTAAAAAGCCAC
 AGGAGTTGAAC TGCTAGGATTCTGACT**ATG**CTGTGGTGGCTAGTGCTCCTACTCCTACCTAC
 ATTAAAATCTGTTTTGTTCTCTTGTAACTAGCCTTACCTTCAACACAGAGGATCTGT
 CACTGTGGCTCTGGCCAAACCTGACCTCACTCTGGAACGAGAACAGAGGTTCTACCCAC
 ACCGTCCCCTCGAAGCCGGGACAGCCTCACCTGCTGGCCTCTCGCTGGAGCAGTGCCCTC
 ACCAACTGTCTCACGTCTGGAGGCAGTGACTCGGGCAGTCAGTAGCTGAGCCTTTGGTA
 GCTGCGGCTTCAAGGTGGCCTTGCCCTGGCGTAGAAGGGAT**TGA**CAAGCCGAAGATT
 CATAGGCAGATGGCTCCACTGCCAGGCATCAGCCTTGCTGTAGTCATCACTGCCCTGGGG
 CCAGGACGGGCCGTGGACACCTGCTCAGAACGAGTCAGTGGGTGAGACATCACGCTGCCGCCAT
 CTAACCTTTCATGTCCGCACATCACCTGATCCATGGCTAAATCTGAACCTGTCCCCAAGG
 AACCCAGAGCTTGAGTGAGCTGTGGCTCAGACCCAGAACGGGTCTGCTTAGACCACCTGGTT
 TATGTGACAGGACTTGACATTCTCCTGGAACATGAGGGAACGCCGGAGGAAAGCAAAGTGGCA
 GGGAAAGGAACTTGTGCCAAATTATGGGTCAAGAAAAGATGGAGGTGTTGGTTATCACAAGGC
 ATCGAGTCTCCTGCATTCACTGGACATGTGGGGAAAGGGCTGCCGATGGCGATGACACACT
 CGGGACTCACCTCTGGGCCATCAGACAGCCGTTCCGCCCGATCCACGTACAGCTGCTG
 AAGGGCAACTGCAGGCCGATGCTCTCATCAGCCAGGCAGCAGCCAAATCTGCGATCACCAG
 CCAGGGCAGCGTCTGGGAAGGAGCAAGCAAAGTGACCATTTCTCCTCCCTCCCTC
 TGAGAGGCCCTCTATGTCCTACTAAAGCCACCAGCAAGACATAGCTGACAGGGCTAATG
 GCTCAGTGTGGCCAGGAGGTCAAGCAAGGCCTGAGAGCTGATCAGAAGGGCTGCTGTGCG
 AACACGGAAATGCCTCCAGTAAGCACAGGCTGAAAATCCCCAGGCAAAGGACTGTGTGGCT
 CAATTAAATCATGTTCTAGTAATTGGAGCTGTCCCCAAGACCAAAGGAGCTAGAGCTTGGT
 TCAAATGATCTCCAAGGCCCTATAACCCAGGAGACTTGTATTGAAACCCCCAAA
 TCCAAACCTAAGAACCGAGGTGCATTAAGAACATCAGTTATTGCCGGGTGTGGTGGCTGTAATG
 CCAACATTTGGGAGGCCGAGGCCGGTAGATCACCTGAGGTCAAGACAGCAGCCTG
 GCCAACATGGTGAACCCCTGTCTACTAAAAATACAAAAAAACTAGCCAGGCATGGTGGT
 GTGTGCCTGTATCCCAGCTACTCGGGAGGCTGAGACAGGAGAATTACTTGAACCTGGGAGGT
 GAAGGAGGCTGAGACAGGAGAATCACTCAGCCTGAGCAACACAGCGAGACTCTGTCTCAGA
 AAAAATAAAAAAAGAATTATGGTTATTTGTAA

FIGURE 170

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71277
><subunit 1 of 1, 109 aa, 1 stop
><MW: 11822, pI: 8.63, NX(S/T): 0
MLWWLVLLLLPTLKSVFCSLVTSLYLPNTEDLSLWLWPKPDLHSGTRTEVSTHTVPSKPGTA
SPCWPLAGAVPSPTVSRLTRAVQVAEPLGSCGFQGGPCPGRRD
```

Signal peptide:

amino acids 1-15

FIGURE 171

GCGGGCCCGCAGTCCGAGACCTGTCCCAGGAGCTCCAGTCACGTGACCTGTCACTGCCTC
 CCGCCGCCTCCTGCCCGGCCATGACCCAGCCGGTCCCCGGCTCTCCGTGCCCGCCGCT
 GGCCCTGGGCTCAGCCGCACTGGCGCCCTCGCCACTGGCCTCTCCTGGGGAGGCGGT
 GCCCCCATGGCGAGGCCGGCGAGAGCAGTGCCTGCTCCCCCGAGGGACAGCCGCTGTGG
 CAGTATCTTCTGAGCCGCTCCATCGGGAGCACCCGGCGTGCAGGCTGAGGCTGCTGAC
 CCTGGAGCAGCCGAGGGGATTCTATGATGACCTGCGAGCAGGCCAGCTTGGCCAACC
 TGGCGGGCTCATCCAGGCCAAGAACGGCGCTGGACCTGGCACCTCACGGCTACTCCGCC
 CTGGCCCTGGCCCTGGCGCTGCCCGGGACGGCGCGTGGTACCTGCGAGGTGGACGCGCA
 GCCCCGGAGCTGGGACGGCCCCGTGGAGGCAGGCCGAGGCCGAGCACAAAGATCGACCTCC
 GGCTGAAGCCGCCTGGAGACCTGGACGAGCTGCTGGCGGGCGAGGCCGGCACCTTC
 GACGTGGCCGTGGTGGATGCGGACAAGGAGAACTGCTCCGCCTACTACGAGCGCTGCCTGCA
 GCTGCTGCGACCCGGAGGCATCCTCGCCGTCTCAGAGTCCTGTGGCGCGGAAGGTGCTGC
 AACCTCCGAAAGGGACGTGGCGCCGAGTGTGCGAAACCTAAACGAACGCATCCGGCGG
 GACGTCAAGGTCTACATCAGCCTCCTGCCCTGGCGATGGACTCACCTGGCCTCAAGAT
 CTAGGGCTGGCCCTAGTGAGTGGCTCGAGGGAGGGTTGCCTGGAACCCCAGGAATTGAC
 CCTGAGTTTAAATTGAAAATAAGTGGGGCTGGGACACAAAAAAA

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FIGURE 172

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71282
><subunit 1 of 1, 262 aa, 1 stop
><MW: 28809, pI: 8.80, NX(S/T): 1
MTQPVPRLSVPAALALGSAALGAAFATGLFLGRRCPPWRGRREQCLLPPEDSRLWQYLLSRS
MREHPALRSLRLLTLEQPQGDSSMTCEQAQLLANLARLIQAKKALDLGTFTGYSALALALAL
PADGRVVTCLEVDAQPPELGRPLWRQAEAEHKIDLRLKPALETLDELLAAGEAGTFDVAVVDA
DKENCSAYYERCLQLLRPGGILAVRLVLWRGKVLQPPKGDVAAECVRNLNERIRRDVRVYIS
LLPLGDGLTLAFKI
```

Important features of the protein:

Signal peptide:

amino acids 1-25

Transmembrane domains:

amino acids 8-30, 109-130

N-glycosylation site.

amino acids 190-193

Tyrosine kinase phosphorylation site.

amino acids 238-246

N-myristoylation sites.

amino acids 22-27, 28-33, 110-115, 205-210, 255-260

Amidation sites.

amino acids 31-34, 39-42

FIGURE 173

CCGCCGCCGAGCCGCTACCGCCGCTGCAGCCGCTTCCGCCGCTGGGCCTTCGCCGTCA
 GC**ATG**CACACGCCCTCAAGCCCCGGGACTTGGTGGCTAAAGATGAAGGGCTACCCCTCAC
 TGGCTGCCAGGATCGACGACATCGCGATGGGCCGTGAAGCCCCCACCAACAAGTACCC
 CATCTTTCTTGGCACACACGAAACAGCCTCTGGGACCCAAGGACCTGTTCCCCTACG
 ACAAAATGTAAAGACAAGTACGGGAAGCCAAACAAGAGGAAAGGCTCAATGAAGGGCTGTGG
 GAGATCCAGAACAAACCCCCACGCCAGCTACAGGCCCTCCGCCAGTGAGCTCCGACAG
 CGAGGCCCCCGAGGCCAACCCCGCCGACGGCAGTGACGCTGACGAGGACATGAGGACCGGG
 GGGTCATGGCCGTACAGCGGTAAACGCCACAGCTGCCAGCGACAGGATGGAGAGCGACTCA
 GACTCAGACAAGAGTAGCGACAAACAGTGGCCTGAAGAGGAAGACGCCCTGCCCTAAAGATGTC
 GGTCTCGAAACGAGCCCAGAAGGCCCTCAGCGACCTGGATCAGGCCAGCGTGTCCCCATCCG
 AAGAGGAGAACTCGGAAAGCTCATCTGAGTCGGAGAAGACCAGCGACCAGGACTTCACACCT
 GAGAAGAAGCAGCGGTCCGGCGCCACGGAGGGCCCTCTGGGGGAGGAAAAAAAGAA
 GGCGCCGTCAAGCTCCGACTCCAAGGCCGATTGGACGGGCCAAGCCTGAGCCGG
 TGGCCATGGCGCGGTCCGGCTCCTCCTCTCCTCTCCTCTCCCTCCGACTCCGATGTG
 TCTGTGAAGAACGCTCCGAGGGGCAGGAAGCCAGCGAGAAGCCTCTCCGAAGCCCGGAGG
 GCGGAAACCGAAGCCTGAACGCCCTCCGTCCAGCTCCAGCAGTGACAGTGACAGCGACGAGG
 TGGACCGCATCAGTGAGTGGAAAGCGCGGGACGAGGCAGGGCAGCTGGAGGGCCCG
 CGCGCGAGAGCAGGAGGAGCTGCAGCGCTCGGGAGCAGGAGAAGGAGGAGAAGGA
 GCGGAGGCAGCGAGCGGGCGACCCGCGGGAGGCTGAGCGGGCAGCGGGCAGCAGCGGG
 ACGAGCTCAGGGAGGACGATGAGCCGTCAAGAACGGGGACGCAAGGGCCGGGGGG
 CCCCCGTCCCTCTGACTCCGAGCCCGAGGCGAGCTGGAGAGAGAGGCCAAGAAATCAGC
 GAAGAACCGCAGTCCTCAAGCACAGAGCCGCCAGGAAACCTGGCCAGAACGGAGAAGAG
 TGCAGGCCGAGGAGAACAGCAAGCCGTGAAGGTGGAGCGGACCCGGAAGCGGTCC
 GAGGGCTTCGATGGACAGGAAGGTAGAGAACAGAACAGGCCCTCCGTGGAGGAGAACG
 GCAGAACGCTGCACAGTGAGATCAAGTTGCCCTAAAGGTGCACAGCCGGACGTGAAGAGGT
 GCCTGAATGCCCTAGAGGAGCTGGAACCCCTGCAGGTGACCTCTCAGATCCTCCAGAAC
 ACAGACGTGGTGGCCACCTTGAAGAACGATTGCCGTTACAAAGCGAACAGGACGTAATGGA
 GAAGGCAGCAGAACGAGTCTATAACCCGGCTCAAGTCGGGGCTCTGGCCCCAAAGATCGAGGCGG
 TGCAGAAAGTGAACAAGGCTGGATGGAGAACGGAGAACGCCAGGAGAACAGCTGGCCGGGGAG
 GAGCTGGCCGGGGAGGAGGCCCCCAGGAGAACGGGGAGGACAAGCCACCGATCTCTC
 AGCCCCAGTGAATGGCGAGGCCACATCACAGAACGGGGAGAGCGCAGAGAACAGGAGCACG
 AGGAGGGTGGACTCGGAGGAGGGCAAGGTGGCTCTGAAGACCTGCACGACAGC
 GTACGGGAGGGTCCGACCTGGACAGGCCCTGGAGCGACGGCAGGAGCGAGAGGGCAGC
 GGGGGACTCGGAGGCCCTGGACGAGGAGAGCT**TGA**GGCGGGCAGCCAGGCCAGCCCCCGC
 CCGAGCTCAGGCTGCCCTCTCCTCCCCGGCTCGCAGGAGAGCAGAGCAGAGAACGTGG
 GAACGCTGTGCTGTTGATTTGTTCCCTGGGTTTTTCTGCCTAATTCTGTGATT
 TCCAACCAACATGAAATGACTATAACGGTTTTAATGA

FIGURE 174

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71286
><subunit 1 of 1, 671 aa, 1 stop
><MW: 74317, pI: 7.61, NX(S/T): 0
MPHAFKPGDLVFAKMKGYPHWPARIDDIADGAVKPPPNKYPPIFFFGTHETAFLGPKDLFPYD
KCKDKYGKPNKRKGFnEGLWEIQNNPHASYSAPPVSSSDSEAPEANPADGSDADEDDERG
VMAVTAVTATAASDRMESDSDSDKSSDNGLKRKTALKMSVSKRARKASSLDQASVSPSE
EENSESSSESEKTSQDFTPEKKAAVRAPRRGPLGGRKKKKAPSASDSDSKADSDGAKPEPV
AMARSASSSSSSSSSDSDVSVKPPRGRKPAEKPLPKPRGRKP PERPPSSSSDSDSDEV
DRISEWKRRDEARRRELEARRREQEEELRLREQEKEEKERRERADRGEAERGSGGSSGD
ELREDDEPVKKRGRKGRGRGPPSSSDSEPEAELEREAKKSAKKPQSSSTE PARKPGQKEKRV
RPEEKQQAKPVKVERTRKRSEGFSMDRKVEKKKEPSVEEKLQKLHSEIKFALKVDSPDVKRC
LNALEELGTLQVTSQILQKNTDVVATLKKIRRYKANKDVMEEKAEVYTRLKSRLGPKIEAV
QKVNKAGMEKEKAEEKLAGEELAGEEAPQEKAEDKPSTDLSAPVNGEATSQKGESAEDKEHE
EGRDSEEGRCGSSEDLHDSVREGPDLDRGSDRQERERARGDSEALDEES

Signal peptide:

amino acids 1-13

FIGURE 175

GTTGGTTCTCCTGGATCTCACCTACCAACTGCAGATCTGGGACTCATCAGCCTCAATAATTATATTAAATTA
 ACACCATTGAAAGAGAACATTGTTTCATCAT**ATGA**ATGCTAATAAAGATGAAAGACTTAAAGCCAGAACCAAGA
 TTTTCACCTTTCTGCTTGATGATGCTAAGCATGACCAGTGTGTTCTCCAGTCAGTGGCACTTTGAAGCA
 AAATATTCCAAGACTCAAGCTAACCTACAAAGACTGCTGCTTCAAATAGCTGTATCCCTTTGGGTTCATC
 AGAAGGACTGGATTTCAAACTCTTCTTAGATGAGGAAAGAGGCAGGCTGCTTGGGAGCCAAAGACCACAT
 CTTTCTACTCAGCTGGTGACTTAAACAAAATTAAAGAAGATTATTGGCCTGCTGCAAAGGAACGGTGG
 ATTATGTAATTAGCTGGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAA
 AACTCACATATATGTTGAGCATTCTACATCCAATATGTTGGTATATTGATCTTGGAGTCTACAAGGA
 GGATATTATATTCAAACATAGACACACATAATTGGAGTCTGGCAGACTGAAATGTCCTTCGATCCTCAGCAGCC
 TTTGCTTCAGTAATGACAGATGAGTACTCTACTCTGGAAACAGCTCTGATTTCTGGCAAAGATACTGCTT
 CACTCGATCCCTGGGCCTACTCATGACCAACACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGG
 AGCAAATTATTGGAACTTCTTCATACCGACACACTACAATCCAGATGATGATAAAATATTCTTCTTCG
 TGAATCATCTCAGGCAAGGACTACCTCCGATAAAACCATCTTCGAGTTGGAAGAGTTGTAAGAATGATGT
 AGGAGGACAACGCAGCTGATAAAACAAGTGGACACTTTCTTAAGGCCAGACTGATTGCTCAATTCTGGAAAG
 TGATGGGAGATACTTACTTGTGAGCTTCAAGATATTATTACTCCCCACAAGAGATGAAAGAAATCTGT
 AGTATATGGAGTCTTACTACAACCAGCTCCATCTCAAAGGCTCTGCTGTTGTGTATAGCATGGCTGACAT
 CAGAGCAGTTTAAATGGTCCATATGCTCATAGGAAAGTGAGCAGACCATCGTTGGTGCAGTATGATGGGAGAAT
 TCCTTATCCACGGCCTGGTACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCACCCGAGATTTCCAGA
 TGATGTCATCAGTTCTCATAAAGCGGCACTCTGTGATGTATAAGTCGTATACCCAGTTGCAAGGAGGACCAACGTT
 CAAGAGAATCAATGTGATTACAGACTGACACAGATAGTGGGAGTATGTCATTGAGAAGATGGCAGTACGA
 TGTAAATGTTCTTGGAAACAGACATTGGAACTGTCCTCAAAGTTGTCAGCATTTCAAAGGAAAGTGGAAATATGG
 AGAGGTAGTGTGAGGAGTTGAGATATTCAAGCACTCATCAATCATCTGAACATGGAATTGTCCTGAAGCA
 GCAACAAATTGTACATTGGTCCCAGATGGATTAGTTGAGCTCTCTGACAGATGCGACACTATGGGAAAGC
 TTGCGCAGACTGTTGCTTGGCAGAGACCCCTACTGTGCTGGATGGAATGCACTGCTCTGATATGTCCTAC
 TTCTAAAAGGAGAGCTAGACGCCAAGATGTAATTGGCACCACATCAGGCTGCTGGACATCGAAGACAG
 CATTAGTCATGAAACTGCTGATGAAAAGGTGATTGGCATTGAAATTAACTCAACCTTCTGGAATTGTCCTGAAGCA
 TAAATCCCAACAAGCAACTTAAATGGTATATCCAGAGGTGAGGGGATGAGCATCGAGAGGAGTTGAAAGCCGA
 TGAAAGAATCATCAAAACGGAATATGGCTACTGATTGAGAAGTGTGGGATGTATTACTG
 CAAAGCCCAGGAGCACACTTCTACATCCACACCATAGTGAAGCTGACTTGAATGTCATTGAGAATGAAACAGATGGA
 AAATACCCAGAGGGCAGAGCATGAGGAGGGCAGGTCAAGGATCTATTGGCTGAGTCACGGTTGAGAATACAAGA
 CTACATCCAATCCTAGCAGGCCAAACTTCAGCTCGACCACTACTGCGAACAGATGTCGACAGGAGAAGCG
 GAGACAGAGAAACAAGGGGGCCCAAAGTGGAAAGCACATGCAAGGAAATGAGAAGAAACGAAATCGAAGACATCA
 CAGAGACCTGGATGAGCTCCCTAGAGCTGAGCCACG**TAG**TTTCTACTTAAATTAAAGAAAAGAATTCTTAC
 TATAAAACATTGGCTTCTGTTGTATATCCCTATAGTAAATTCAAAATGCTCCATGGAGTTGCTAAGG
 CACAAGACAATACTGAATAAGACAATATGTGATGAATATAAGAAAGGCAAAAATTCAATTGAAACCAGTT
 CCAAGAACAAATCTGCACAAGCAAAGTATAAGAATTATCTCTAAAATAGGGGTTACAGTTGAAATGTT
 TGTTTGAGTTTGGAAATTATTGTCATGTAATAGTTGAGCTAAGCAAGCCCGAATTGATAGTGTATAAGG
 GCTTTATTCCCTGAAATGTCCTAAAGCATGGAATTACCATGCGAGTTGCTATGTCCTTATGAACAGATAT
 CATTCCATTGAGAACAGCTACCTGGTAGGGATAAGAGCTCAGACACAAATTAAAGACAATCCCATTATC
 AACAGGAACCTCTCAGTGAGGACATTCACTCCTGGAGAATGGTATAGGAATTGGAGAGGTGCATTATTCTTC
 TGGCCACTGGGTTAAATTAGTGTACTACAACATTGATTACTGAAGGGCAACTATGTTCCCCCAGGATTCT
 ATTGACTAGTCAGGAGTAACAGGTTCACAGAGAGAAGTGGTGCCTAGTTGTTTAGAGTATATACTAA
 GCTCTACAGGGACAGAACATGCTTAAATAACTTAAAGATATGGGAAATTGTTAAACAAAGGAAACA
 TAATGATGTATAATGCATCCTGATGGGAAGGCATGAGATGGGATTGTTAGAAGACAGAAGGAAAGACAGCCAT
 AAATTCTGGCTTGGGAAAACCTCATATCCCCATGAAAAGGAAGAACAAATCAAATAAGTGGAGACTATGAA
 TGGAGCTTTTCACTAGGGTATAAGTAGCTGCCAATTGTAATTCATCTGTTAAAAAAATCTAGATTATAACA
 AACTGCTAGCAAAATCTGAGGAAACATAAATTCTCTGAAGAATCATAGGAAGAGTAGACATTATTATAACC
 AATGATATTCTCAGTATATATTCTCTCTTTAAAAAAATTATTCATACACTCTGTATATTATTCTTTTACTGC
 CTTTATTCTCCTGTATATTGGATTGTTGATTATATTGAGTGAATAGGAGAAAACAATATAACACACAGA
 GAATTAGAAAATGACATTCTGGGAGTGGGATATATATTGTTGAATAACAGAACGAGTGTAAAATTAAAC
 AACGGAAAGGGTTAAATTAAACTCTTGACATCTTCACTCAACCTTTCTCATTGCTGAGTTAATCTGTTGTAATT
 GTAGTATTGTTTGTAAATTAAACAATAAGCCTGCTACATGT

FIGURE 176

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71883
><subunit 1 of 1, 777 aa, 1 stop
><MW: 89651, pI: 7.97, NX(S/T): 3
MNANKDERLKARSQDFHLFPALMMLSMTMLFLPVTGTLKQNIPLKLTYKDLLLLNSCIPFL
GSSEGLDFQTLLLDEERGRLLLGAHDHIFLLSLVDLNKNFKKIYWPAAKERVELCKLAGKDA
NTECANFIRVLQPYNKTHIYVCGTGFHPICGYIDLGVYKEDIIFKLDTHNLESGRLKCPFD
PQQPFASVMTDEYLSTGTASDFLGKDTAFTRSLGPTHDDHYIRTDISEHYWLNGAKFIGTFF
IPDTYNPDDDKIYFFFRESSQEGSTSDFKTIISRVGRVCKNDVGGQRSLINKWTTFLKARLIC
SIPGSDGADTYFDELQDIYLLPTRDERNPVVYGVFTTSSIFKGSAVCVYSMADIRAVFNGP
YAHKESADHRWVQYDGRIPYPRPGTCPSKTYDPLIKSTRDFPDDVISFIKRHSVMYKSVYPV
AGGPTFKRINVVDYRLTQIVVDHVNIAEDGQYDVMFLGTDIGTVLKVVSIKEKWNMEEVLE
LQIFKHSSIILNMELSLKQQQLYIGSRDGLVQLSLHRCDTYKGACADCCLARDPYCAWDGNA
CSRYAPTSKRRARRQDVKYGDPIQCWDIEDSISHEADEKVIFGIEFNSTFLECIPKSQQA
TIKWIYIQRSGDEHREELKPDERIYKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLN
VIENEQMENTQRAEHEEGQVKDLLAESRLRYKDYIQILSSPNFSLDQYCEQMWHREKRRQRN
KGGPKWKHMQEMKKRNRRHHRDLDLPRAVAT
```

Important features of the protein:**Signal peptide:**

amino acids 1-36

N-glycosylation sites.

amino acids 139-142, 607-610, 724-727

Tyrosine kinase phosphorylation site.

amino acids 571-576

Gram-positive cocci surface proteins 'anchoring' hexapeptide.

amino acids 32-37

FIGURE 177

CCCTGACCTCCCTGAGCCACACTGAGCTGGAAGCGCAGAGGTATCCTGGAGCATGCCACCAGCGGGGAGCAGA
 CAACCTCCCAGGTAAAGCTGGAGCAAGACCTGAAGCTGTTCTCAGGAGCCTGGTGTATTTCCCCCACCCAC
 CTCAGCAGTTCAGCCAGCAGGGACTGATCAGGTGTGTCTGGAGTGGGAGCAGAAGGCCTGGCTGGCAAGA
 GTGGCCTGGAGAAAGAGGTTAGCGCTTGACAGCCAGCTGCCGTGACTACAAGATCCAGAACCATGGGCATC
 GGGTAGGGTGGGGGGCACAGGTGTATGTGCACCTTCTGTCTCAGCAAGAACAGCTGAGAGAGGGGATCTGG
 AGCCATTGAGGGTGTATGGAGCTACAGAGGGAGGGAAAGGTATTTAAGGTAAACAGTGTGGCACAAATAGTTAA
 GAGCACAGTTTGGAGCTAGACGACATAGGTCAAATTCTCTGTGCTTCTAGTCTGAGCCCCAGGT
 AAGGGAGTGAATTAACCTCTGACTCAATTCTCATCACTAAAGTAGGGCCAATAATAGCACCCACCTCAT
 AGGAAAGATTAATGACATAATGTATGTG**ATG**CAACTAGCAAAGTACCACTGGAGCAGAGGGGGCAGGCTT
 TATTTCCACCCACCCCTGTTCTGCCCCACCCAGGTACTGCAACGACTGGAGCAGAGGGGGCAGGCTT
 CAGAGCGGGAGGCTCCAAGCATAGAACAGAGGTACAGGAAGTGCGAGAGAGCATCCGCCGGCACAGGTGAGCC
 AGGTGAAGGGGCTGCCGGTGGCCCTGCTCAGGGGGCTGGCTTAGATGTGGAGCGCTGGCTGAAGCCAGCCA
 TGACCCAGGCCAGGATGAGGTGGAGCAGGAGCGGGCTCAGTGAGGCTCGGCTGCCCAGAGGGACCTCTC
 CAACCGCTGAGGATGCTGAGCTTCTGACTTTGAGGAATGTGAGGAGACGGGAGAGCTCTTGAGGAGCCTGCC
 CCCAAGCCCTGGCACGAGGCCCTCCCTGCCCTGCACACGTGTTATTCGCTATCAGGCAGGGCGTGAGGATG
 AGCTGACAATCACGGAGGGTAGTGGCTGGAGGTATAGAGGGAGATGCTGACAATGGGCAAGGCTCGGA
 ACCAGCACGGCGAGGTAGGCTTGTCCCTGAGCGATATCTCAACTTCCCGAACCTCTCCCTCCAGAGAGCAGCC
 AAGACAGTACAATCCCTGCCGGCAGAGCCCACAGCATTCTGGCACAGGCCCTGTACAGCTACACCGGACAGA
 GTGCAGAGGAGCTGAGCTTCCCTGAGGGGCACACTCATCCGTCTGCTGCCCGGGCCAAGATGGAGTAGATGACG
 GCTTCTGGAGGGAGAATTGGGGCCCTGTTGGGGCTTCCCTGCTGGTGAAGAGCTGCTTGGCCCC
 CAGGGCACCTGAACCTCTGACCCCTGAACAGATGCTGCCCTCCCTCCTCCAGCTTCCCTGGGACCTGCAC
 CTACCTCTGTGTTGGATGGGCCCCCTGACCTGTCTGCCCTGGGACAAGCCCTGACTTCCCTGGGTTCTGG
 ACATGATGGCACCTCGACTCAGGCCATGCGTCCACCACCTCCCCGGCTAAAGCCCCGGATCTGGGCCACC
 CAGATCCCCTCACCT**TGA**AGGCCAGGGAGCCTTGACCCCGTGTGCTGCTGCTCCATCTCAAGCTGTCAGA
 CCACACCATCAATGATCCAGAGCAACACGCCAAAAGCTGGAATGCCCTTATTCACCCCTCACCTCCAAGGGT
 GGAAACTTGCCCTCCCATTCTAGAGCTGGAACCCACTCCCTTTTCCATTGTTCTATCATCTTAGGACC
 GGAACTACTACCTCTCTGTGACCCCTATCTAGGGTGTGAAATGCTGAAATCTCTGGGCTGGAAACC
 ATCCATCAAGGTCTCTAGTAGTTCTGCCACCTCTTCCCAACCTGGCTCCATGACCCACCCACTCTGGATG
 CCAGGGCACTGGGCTGGGCTGGGAGAGGAACAGGCCCTGGAATCAGGAGCTGGAGCCAGGATGCGAACGAG
 CTGTAATGGCTGAGGGATTATTGACAATGAATAAGGGCACGAAGGCCAGGGCAGGGCTGGGCTCTGTG
 CTAAGAGGGCAGGGGGCTACGGTGTATTGCTTAGGGGCCACACGGGCAGGGCCTGCTCCAGCTGCCAC
 GCTCTATCATATGGAGCGAGGTGTTGGGGAAAGCGGGGAGGCAGCCTGTTGCAAGGCAGGGGAAGGAGAAC
 TGAGGGCTGTGACCTCTGAGGCCCTCAGCCTGAGACTGTGCAACTCCAGGTGAAAGTAGAGCTGGTCCCTC
 AGCTGGGGCAGTGTGTCAGTGGAGGGAGGGCTTCAGGCCACCCACCCCTGGCCCTGCCAGCTGGTAG
 TCCATCAGCACAATGAAGGAGACTTGGAGAAGAGGAAGAAATAACACTGTTGCTTCTGTTCAAGCTGTGTCAGC
 TTTCCCTGGGCTCCAGGACCTCCACCTCACCAACCAAGGGATTATAGCAAAGGCTAACGCTGC
 AGTTTACTCTGGGGGTACGGAGGCCAAAGGCTTAAATAGTTAAGTAGGTGATGGAAGATGAGATTACCTCA
 TTTAGGGCTCAGGAGACTCACCTCACATACTCCCTGCTCCCTGTGGTAGAGACACCTGAGAGAAAGGGAGGG
 TCAACAATGAGAGACCAGGGTAGGGCTATCAGTGCCCTCAGACTGAGAGAGCAATAAGAGCCAGCCAGTC
 AGTCCCGGCTGTGTTCTACCTGGTGTACAGAAGTGTCTGGCTGCCCATTGCTCTGAGTGG
 GCAGCCCTGGCTGGGCCCCCTCCCTCCGGCTCAGTGTGGCTTGCTGAGAAGCTGGGGTCCCTCAAGTG
 CACGAGGGTTAGGGTGTGCTCCCTGAGCTCCATTCTGTACTGGGGCTGGCTAGGACCTGGGGCTGGGCC
 TCTCAGGGGGCAGCTCTCCATGGCAGGCATCCCTGCCCTGGCTGCCCTCCCCAGACCCCTGACCACCCCTG
 GGTCTGTCCCCCACCAGGCCAGCTCTGTCTGTGGGGAGCCATCACGGTGTGCACTGCCATAGCGCT
 TCTCAATGTGTGTCACCGGAACCTGGAGGGAGGGAAACACTGGGGTTAGGACCAACTCAGAGGCTGTTG
 GCCCTCCCTGACCAAGGGACATCCTGAGTTGGCTACTTCCCTGAGGCTAACGGTAGGGAGGCCTCTC
 AGATTGTGGGGCACATTGTGTAAGCCTGACTCTGCTGGAGCTCCAGTCCAGGAGGAAGAGCAAGGCCACTT
 TTGGGATCAGGTGCTGATCACTGGGCCCCCTACCTCAGCCCCCTTCCCTGGAGCACCTGCCCACTGCCCA
 CAGAGAACACAGTGGCTCCCTGTCGGGGGGCGGTTTCCCTGAGGCGTCCCTGACGGACAAGTGGAG
 GCCTCTGCTGCCGTGCAATGGATGCAAGGGCTGCAGAGCCCAGGTGCACTGTGATGATGGAGGGGCTC
 CGTCCTGCAGGCTGGAGGTGGCATCCACACTGGACAGCAGCAGGAGGAGGGAGTGAGGGTAACATTCCATT
 TCATGTTGTTCTACGTTCTGAGCATGCTCTTAAACCCAGAACGCCAATTGCCAAGGCCATT
 TTTCTGCTTTATCTAAACTCAATTAAG

FIGURE 178

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73401
><subunit 1 of 1, 370 aa, 1 stop
><MW: 40685, pI: 4.53, NX(S/T): 0
MQLAKYQSHSKSCPTVFPPTPVLCLPNQVLQRLEQRQQASEREAPSIEQRLQEVRESIRRA
QVSQVKGAARLALLQGAGLDVERWLKPAMTQAQDEVEQERRLSEARLSQRDLSPTAEDAELS
DFEECEETGELFEEPAPQALATRALPCPAHVVFRYQAGREDELTTITEGEWLEVIEEGDADEW
VKARNQHGEVGFVPERYLNFPDLSLPESSQDSDNPCGAEPTAFLAQALYSYTGQSAEELSFP
EGALIRLLPRAQDGVDGFWRGEFGGRGVFPSLLVEELLGPPGPPELSDPEQMLPSPSPPS
FSPPAPTSVLDGPPAPVLPGDKALDFPGFLDMMAPRLRPMRPPPPPAAKAPDPGHPDPLT
```

FIGURE 179A

CACAGGGAGACCCACAGACACATATGCACGAGAGAGACAGAGGGAGGAAAGAGACAGAGACAAAGGCACAGCGGAA
 GAAGGCAGAGACAGGGCAGGCACAGAACGGCCAGACAGAGTCCTACAGAGGGAGAGGCCAGAGAACGCTGCAGA
 AGACACAGGCAGGGAGAGACAAAGATCCAGGAAGGGAGGCTCAGGGAGAGTTGGAGAACCCAGACCCCTGG
 GCACCTCTCCAAGCCCAGGACTAAGTTTCTCCATTCTTAACGGCTCAGCCCTCTGAAAACCTTGCC
 TCTGACCTTGGCAGGAGTCAAGCCCCAGGCTACAGAGAGGAGCTTCAAAGCTAGGGTGTGGAGGACTTGGT
 GCCCTAGACGGCCTCAGTCCCTCCAGCTGCAGTACCAAGTGCATGTCCAGACAGGCTCGCATCCCAGGGAGGG
 CTTGGCAGGGCGCTGGCTGTGGGAGCCAACCCCTGCCTCTGGCATTGTGCCGCTCTCTGGCTGGTGTG
 GCTGCTCTGCTACTGCTGGCTCTCTGGCCCTCAGGCCAGCGTCCGGCTGGCTGGGAGGAGGAGAT
 CGTGTTCAGAGAACGCTCAACGGCAGCGTCCGGCTGGCTGGGAGGAGGAGTGGCTGAGGGCTGACAGTGCAGTA
 GGCCTTGGGAGACGCTGACTAGAGCTGGAGCAGGACTCCGGTGTGCAGGTCAGGGCTGACAGTGCAGTA
 CCTGGGCCAGGCCTGAGCTGCTGGTGGAGCAGAGCCTACACTGACTGGCACCATCAATGGAGATCC
 GGAGTCGGTGGCATCTGCACGGATGGGAGGCCCTGTTAGGCGTGTACAATATCGGGGGCTGAACCTCA
 CCTCCAGCCCCCTGGAGGGAGGCACCCCTAACTCTGCTGGGGACCTGGGCTCACATCCTACGCCGAAGAGTCC
 TGCCAGGGTCAAGGTCCCATGTGCAACGTCAAGGCTCCTTGGAGGCCAGACCCGAAGAGCCAA
 GCGCTTGCTTCACTGAGTAGATTGTGGAGACACTGGTGGTGGCAGATGACAAGATGGCGCATCCACGGTGC
 GGGGCTAAAGCGTACCTGCTAACAGTGATGGCAGCAGCAGCCAAGGCCCTCAAGCACCAAGCATCCGCAATCC
 TGTCAGCTTGGTGGTACTCGCTAGTGATCCTGGGTGAGGAGGGGCCAAAGTGGGCCAGTGCTGC
 CCAGACCCCTGCGCAGCTCTGCTGCCTGCCAGCGGGCCCTCAACACCCCTGAGGACTCGGGCCCTGACCACCTTG
 CACAGCCTTCTGTTACCCCTCAGGACCTGTGTGGAGTCTCAGTGGCTGACACGCTGGTATGGCTGATGTGG
 CACCGCTGTGACCCGGCTGGAGCTGTGCCATTGTGGAGGATGATGGGCTCCAGTCAGCCTTCACTGCTGCTCA
 TGAACGGGTATGCTTCAACATGCTCATGACAACACTAACGCCATGCACTGATTTGAATGGCCTTGGAC
 CTCTCGCCATGTCAATGGGCTCATGGGACTCATGCTCTTGAAGACAAACAGAGGCTCATTGCACTGCTGCTT
 CATCACTGACTTCTGGCAAAATGGTATGGGACTGTCTTGAAGACAAACAGAGGCTCATTGCACTGCTGCTT
 GACTTTCCCTGGCAAGGACTATGATGCTGACGCCAGTGCACGGCTGACCTTGGGCCGACTCACGCCATTGTCC
 ACAGCTGCCGCCCTGTGCTGCCCTGGTGCTGGCCACCTCAATGGCATGCCATGTGCCAGACCAAACA
 CTCGCCCTGGCCGATGGCACACCCCTGCCGGCCGACAGGCCATGGTGCTGCCCTCACATGGACCA
 GCTCCAGGACTTCAATATTCCACAGGCTGGTGGCTGGGCTTGGGACCATGGGACTGTCTCGGACCTG
 TGGGGTGGTGTCCAGTTCTCCTCCCGAGACTGCACGAGGCCAGTGGCCGAGACTATGTGCTGGAGG
 CCGCGTACCGCTCCGCTCTGCAACACTGAGGACTGCCAACGGCTCAGGCCCTGACCTCCGCGAGGAGCA
 GTGTGCTGCCATCAACCACCGCACCGACCTCTCAAGAGCTCCAGGGCCATGGACTGGGCTCGCTACAC
 AGGCCTGGCCCCCAGGACCAAGTGCACACTCACCTGCCAGGCCGGGACTGGCTACTACTATGTGCTGGAGCC
 ACGGGTGGTAGATGGGACCCCTGTTCCCGAGACTCCTCGGTCTGTGTGCTCCAGGCCGATGCATCCATGCTGG
 CTGTGATGCATCATTGGCTCCAAGAAGATTGACAAGTGATGGTACTGGGAGGGACGGTCTGGTGTGAG
 CAAGCAGTCAGGCTCCTCAGGAAATTCAAGGTACGGATAACAACAATGTGGTACTATCCCCGGGGGCCACCA
 CATTCTGTCCGGCAGCAGGAAACCCCTGGCACCGGAGCATCTACTTGGCCCTGAAGCTGCCAGATGGCTCCTA
 TGCCCTCAATGGTGAATACACGCTGATGCCCTCCCCACAGATGTGGTACTGCCCTGGGCACTCAGCTTGC
 CAGCGGGGCCACTGCCAGAGACACTGCCAGGACACTGCCAGGACACTGCCAGGCCCTTGACACTGCAAGTCC
 AGTGGCTGGCAACCCCGAGGACACGCCCTCCGATACAGCTTCTCGTGGCCGGCCAGGCCCTCAACGCCACG
 CCCCACTCCCCAGGACTGGCTGCCAGGAAGGACACAGATCTGGAGATCTTGGCCGGCCGGGGGGGGGG
 GAAATAAACTCACTATCCCGGCTGCCCTTCTGGGACCCGGCTGGGAGGGACTGGTGGAGAAAGAGAGACTT
 CTGTGCTGCCCTCATGCTAACACTCAGTGGGAGGGCTGTGGGCGTGGAGACCTGCCCTCCTCTGCCCTAAT
 GCGCAGGCTGGCCCTGCCCTGGTTCTGCCCTGGGAGGCAGTGATGGTTAGTGGATGGAAGGGCTGACAGAC
 AGCCCTCCATCTAAACTGCCCTCTGCCCTGCCAGGAGGGGGAGGCAGGGAGGGCCTGGGGCC
 CAGTTGTATTTATTAGTATTATTCACCTTTATTAGCACCCAGGGAGGGGACAAGGACTAGGGCTCTGGGAA
 CCTGACCCCTGACCCCTCATGCCCTCACCTGGGCTAGGAAATCCAGGGTGGTGTGATAGGTATAAGTGGT
 TGTGTATGCGTGTGTGTGTGAAATGTGTGTGCTATGTATGAGGTACAACCTGTTCTGCTTCC
 TTCCCTGAATTATTTATTGGAAAAGAAAAGTCAAGGGTAGGGTGGGCCCTCAGGGAGTGAGGGATTATCTTT
 TTTTTTTCTT
 GCACAATCTCGGCTCACTGCATCCTCCGCCCTCCGGGTTCAAGTGATTCTCATGCCCTCAGCCTCTGAGTAGCT
 GGATTACAGGCTCTGCCACCAGCCCAGCTAATTGGTTGGGAGGAGACAGAGTCTCGTATTGTC
 ACCAGGGCTGGAATGATTCAAGCTCACTGCCACCTGCCACCCAGGCCAGCTAATTGGTTGGGAGGAGACAGAGTCTCGTATTGTC
 CGAGTAGCTGAGATTATAGGCACCTACCAACGCCGGCTAATTGGTTGGGAGGAGTGGGAGTGAGGGATTATCTTCA
 CATGTTGGCCAGGCTGGCTCGAACCTGCCCTAGGTGATCCACTGCCCTCATCTCCCAAAGTGTGGGATT
 ACAGGGCGTGGCCACCGTGGCTGGCCACGCCAACTAATTGGTATTAGTAGAGAGACAGGGTTTACCATGT
 TGGCCAGGCTGCTCTGAACCTCTGACCTCAGGTAATGACCTGCCCTCGGCCCTCCCAAAGTGTGGGATTACAGG
 TGTGAGGCCACCACGCCGGTACATATTAAATTGAATTCTACTATTATGTGATCCTTGGAGTCAGACAG

FIGURE 179B

ATGTGGTTGCATCTTAACCTCCATGTCTCTGAGCATTAGATTTCATTTGCCAATAATAATACCTCCCTAGAAG
TTTGTGAGGATTAAATAATGTAATAAGAAACTAGCATAACACTCAAAAAAAAAAAAAAAAAGGAAA
AAAAAAAAAAAAAAAAGGAAA

FIGURE 180

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73492
><subunit 1 of 1, 837 aa, 1 stop
><MW: 90167, pI: 8.39, NX(S/T): 1
MSQTGSHPGRGLAGRWLWGAQPCLLLPIVPLSWLVWLLLLLASLLPSARLASPLPREEEIV
FPEKLNGSVLPGSAGAPARLLCRLQAFGETLLEQDSGVQVEGLTVQYLQQAPELLGGAEP
GTYLTGTINGDPESVASLHWDDGGALLGVLQYRGAEHLHQPLEGGTPNSAGGPGAHILRRKSP
ASGQGPMCNVKAPLGSPSPRRAKRFASLSRFVETLVVADDKMAAFHGAGLKRYLLTVMAA
AAAKAFKHPSIRNPVSLVVTRVLVILGSGEEGPVQVGPSSAAQTLRSFCAWQRGLNTPEDSGPDHF
DTAILFTRQDLCGVSTCDTLMADVGTVCDPARSCAIVEDDGLQSAFTAAHELGHVFNMLHD
NSKPCISLNGPLSTSRRHMAPVMAHVDPPEPWSPCSARFITDFLDNGYGHCLLDKPEAPLHL
PTVTPGKDYDADRQCQLTFGPDSRHCQQLPPPACAALWCSGHLNGHAMCQTKHSPWADGTPCG
PAQACMGGRCIHMQLQDFNIPOQAGGWGPWGPGDCSRTCGGGVQFSSRDCTRVPVRNGGKY
CEGRRTFRSCNTEDCPTGSALTFREEQCAAYNHRTDLFKSFPGPMDWVPRYTGVAPQDQCK
LTCQARALGYYVLEPRVVDGTPCSPDSSVCVQGRCIHAGCDRIIGSKKKFDKCMVCGGDG
SGCSKQSGSFRKFRYGYNNVTIPAGATHILVRQQGNPGHSIYLAALKLPDGSYALNGEYTL
MPSPTDVVLPGAVSLRYSGATAASETLSGHGPLAQPLTLQVLVAGNPQDTRLRYSFFVPRPT
PSTPRPTPQDWLHRRAQILEILRRRPWAGRK
```

Important features of the protein:**Signal peptide:**

amino acids 1-48

N-glycosylation site.

amino acids 68-71

Glycosaminoglycan attachment site

amino acids 188-191, 772-775

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 182-185

Tyrosine kinase phosphorylation site.

amino acids 730-736

N-myristoylation sites.

amino acids 5-10, 19-24, 121-126, 125-130, 130-135, 147-152, 167-172, 168-173, 174-179, 323-328, 352-357, 539-544, 555-560, 577-582, 679-684, 682-687, 763-768

Amidation sites.

amino acids 560-563, 834-837

Leucine zipper pattern.

amino acids 17-38, 24-45

Neutral zinc metallopeptidases, zinc-binding region signature.

amino acids 358-367

FIGURE 181

CAGCAGTGGCTCTCAGCCTCTCAAAGCAAGGAAAGAGTACTGTGTGCTGAGAGACC**ATGG**
 CAAAGAACCTCCAGAGAATTGTAAGACTGTCACATTCTAAATGCAGAAGCTTTAAATCC
 AAGAAAATATGTAATCACTTAAGATTGTGGACTGGTGTGTTGGTATCCTGCCCTAACTCT
 AATTGTCCTGTTGGGGAGCAAGCACTCTGCCGGAGGTACCCAAAAAGCCTATGACA
 TGGAGCACACTTCTACAGCAATGGAGAGAAGAAGAAGATTACATGAAATTGATCCTGTG
 ACCAGAACTGAAATATTCAAGCGGAATGGCACTGATGAAACATTGAAAGTGCACGACTT
 TAAAAACGGATACTGGCATCTACTCGTGGTCTTCAAAAATGTTTATCAAAACTCAGA
 TTAAAGTGATTCTGAATTTCTGAACCAGAAGAGGAAATAGATGAGAATGAAGAAATTACC
 ACAACTTCTTGAAACAGTCAGTGATTGGTCCCAGCAGAAAAGCCTATTGAAAACCGAGA
 TTTCTTAAAAATTCCAAAATTCTGGAGATTGTGATAACGTGACCATGTATTGGATCAATC
 CCACTCTAATATCAGTTCTGAGTTACAAGACTTGGAGGAGGGAGAAGATCTTCACTTT
 CCTGCCAACGAAAAAAAGGGATTGAACAAAATGAACAGTGGTGGTCCCTCAAGTGAAGT
 AGAGAAGACCCGTACGCCAGACAAGCAAGTGGAGAAACTCCAATAATGACTATACTG
 AAAATGGAATAGAATTGATCCCAGTGGATGAGAGAGGTTATTGTTGTATTACTGCCGT
 CGAGGCAACCGCTATTGCCGCCCGTCTGTGAACCTTACTAGGCTACTACCCATATCCATA
 CTGCTACCAAGGAGGACGGAGTCATCTGTCGTGTACATGCCCTGTAAGTGGTGGTGGCCC
 GCATGCTGGGAGGGTC**TAA**TAGGAGGTTGAGCTCAAATGCTTAAACTGCTGGCAACATAT
 AATAAATGCATGCTATTCAATGAATTCTGCCTATGAGGCATCTGCCCTGGTAGCCAGCT
 CTCCAGAATTACTGTAGGTAATTCTCTTCATGTTCTAAACTTACATTATCACC
 AAAAAAAAAAAAAAAA

FIGURE 182

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73727
><subunit 1 of 1, 317 aa, 1 stop
><MW: 37130, pI: 5.18, NX(S/T): 3
MAKNPPENCEDCHILNAEAFSKKICKSLKICGLVFGILALTLIVLFWGSKHFWPEVPKKAY
DMEHTFYSNGEKKKIYMEIDPVTRTEIFRSGNGTDETLEVHDFKNGYTGIYFVGLQKCFIKT
QIKVIPEFSEPEEEIDENEETTTFFEQSVIWVPAEKPIENRDFLKN SKILEICDNVTMYWI
NPTLISVSELQDFEEEEDLHF PAN EKKGIEQNEQWVVPQVKVEKTRHARQASEEELPINDY
TENGIEFDPM LDERGYCCIYCRRGNRYCRRVCEPLLGYYPYCYQGGRVICRVIMPCNWWV
ARMLGRV
```

Important features of the protein:**Signal peptide:**

amino acids 1-40

Transmembrane domain:

amino acids 25-47 (type II)

N-glycosylation sites.

amino acids 94-97, 180-183

Glycosaminoglycan attachment sites.

amino acids 92-95, 70-73, 85-88, 133-136, 148-151, 192-195, 239-242

N-myristoylation sites.

amino acids 33-38, 95-100, 116-121, 215-220, 272-277

Microbodies C-terminal targeting signal.

amino acids 315-317

Cytochrome c family heme-binding site signature.

amino acids 9-14

FIGURE 183

GCAGGAACCTGGCTCCGGCTGGCACCTGAGGAGCGGCGTGACCCGAGGGCCCAGGGAGCTGCC
 CGGCTGGCCTAGGCAGGCAGCCGACC**ATG**GCCAGCACGGCGTGCAGCTCTGGGCTTCCT
 GCTCAGCTTCCTGGGCATGGTGGGCACGTTGATCACCACCATCCTGCCGCACTGGCGGAGGA
 CAGCGCACGTGGGCACCAACATCCTCACGGCGTGCCTACCTGAAAGGGCTCTGGATGGAG
 TGTGTGTGGCACAGCACAGGCATCTACCAAGTGCAGATCTACCGATCCCTGCTGGCGCTGCC
 CCAAGACCTCCAGGCTGCCCGCCCTCATGGTCATCTCCTGCCCTGCCTCGGGCATAGCCT
 GCGCCTGCGCCGTATCGGGATGAAGTGACCGCAGGGCACACCCGCCAAGACC
 ACCTTGCCATCCTCGGCGCACCTCTTCATCCTGCCGCCCTGTGCATGGTGGCGT
 CTCCTGGACCACCAACGACGTGGTGCAGAACATTCTACAACCCGCTGCTGCCAGCGGATGA
 AGTTTGAGATTGGCCAGGCCCTGTACCTGGGCTTCATCTCCTCGTCCCTCGCTCATTGGT
 GGCACCCCTGCTTGCCCTGCCAGGACGAGGCACCCCTACAGGCCCTACCAGGCCCGCC
 CAGGGCCACCACGACCACTGCAAACACCGCACCTGCCCTACCAGCCACCAGCTGCCCTACAAAG
 ACAATCGGGCCCCCTCAGTGACCTCGGCCACGCACAGCGGTACAGGCTGAACGACTACGTG
TGAGTCCCCACAGCCTGCTCTCCCTGGGCTGCTGTGGCTGGTCCCCGGGGACTGTC
 AATGGAGGCAGGGGTTCCAGCACAAAGTTACTTCTGGCAATTTGTATCCAAGGAAATA
 ATGTGAATGCGAGGAAATGTCTTAGAGGCACAGGGACAGAGGGGAAATAAGAGGGAGGAGAA
 AGCTCTCTATACCAAAGACTGAAAAAAAATCCTGTCTGTGTTTGATTTATTATATAT
 TTATGTGGGTGATTGATAACAAGTTAATATAAAGTGACTGGGAGTTGGTCAGTGGGT
 TGGTTTGTGATCCAGGAATAAACCTTGCAGGATGTGGCTGTTATGAAAAAAA

FIGURE 184

MASTAVQLLGFLLSFLGMVGTLITTLPHWRRTAHVGTNILTAVSYLKGLWMECVWHSTGIY
QCQIYRSLLALPQDLQAARALMVISCLLSGIACACAVIGMKCTRCAKGTPAKTTFAILGGTL
FILAGLLCMVAWSWTNDVQNFYNPLLPSGMKFEIGQALYLGFISSSLSLIGGTLCLSCQ
DEAPYR PYQAPPRATT TANTAPAYQPPAAYKDNRAPS VTSATHSGYRLNDYV

Important features of the protein:

Signal peptide:

amino acids 1-21

Transmembrane domains:

amino acids 82-103, 115-141, 160-182

FIGURE 185

GAGCTCCCTCAGGAGCGCGTTAGCTTCACACCTCGGCAGCAGGAGGGCGGCAGCTCTCG
 CAGGCGGCAGGGCGGGCGGCCAGGATC**ATG**TCCACCACCATGCCAAGTGGTGGCGTTCCCT
 CCTGTCCATCCTGGGGCTGGCCGGCTGCATCGCGGCCACCAGGATGGACATGTGGAGCACCC
 AGGACCTGTACGACAACCCGTCACCTCCGTGTTCCAGTACGAAGGGCTCTGGAGGAGCTGC
 GTGAGGCAGAGTTCAGGCTTCACCGAATGCAGGCCATTTCACCACCTGGACTTCCAGC
 CATGCTGCAGGCAGTGCGAGCCCTGATGATCGTAGGCATCGCCTGGGTGCCATTGCCCTCC
 TGGTATCCATCTTGCCCTGAAATGCATCCGATTGGCAGCAGTGGAGGACTCTGCCAAAGCC
 AACATGACACTGACCTCCGGATCATGTTCATTGTCTCAGGTCTTGCAATTGCTGGAGT
 GTCTGTGTTGCCAACATGCTGGTACTAACTTCTGGATGTCCACAGCTAACATGTACACCG
 GCATGGGTGGGATGGTGCAGACTGTTCAGACCAGGTACACATTGGTGGCTCTGTTCGTG
 GGCTGGGTGCGTGGAGGCCTCACACTAATTGGGGGTGTGATGATGTGCATGCCCTGCCGGGG
 CCTGGCACCAAGAAAGAAACCAACTACAAAGCCGTTCTTATGCCTCAGGCCACAGTGGT
 CCTACAAGCCTGGAGGCTTCAAGGCCAGCAGTGGCTTGGGTCCAACACCAAAAACAAGAAG
 ATATACGATGGAGGTGCCGCACAGAGGACGAGGTACAATCTTATCCTTCAAGCACGACTA
 TGTG**TAAT**GCTCTAAGACCTCTCAGCACGGCGGAAGAAACTCCGGAGAGCTCACCCAAAA
 AACAAAGGAGATCCCCTAGATTCTTCTGCTTGACTCACAGCTGGAAAGTTAGAAAAGC
 CTCGATTTCATCTTGAGAGGCCAAATGGTCTTAGCCTCAGTCTGTCTCAAATATTCC
 ACCATAAAACAGCTGAGTTATTATGAATTAGAGGCTATAGCTCACATTTCAATCCTCTAT
 TTCTTTTTAAATATAACTTCTACTCTGATGAGAGAATGTGGTTAATCTCTCTCAC
 ATTTTGATGATTAGACAGACTCCCCCTCTCCTCTAGTCATAAAACCCATTGATGATCTA
 TTTCCAGCTTATCCCCAAGAAACTTTGAAAGGAAAGAGTAGACCCAAAGATGTTTTT
 CTGCTGTTGAATTGTCTCCCCACCCCAACTGGCTAGTAATAAACACTTACTGAAGAA
 GAAGCAATAAGAGAAAGATATTGTAATCTCCAGGCCATGATCTGGTTTCTACACTG
 TGATCTAAAAGTTACCAAACCAAAGTCATTTCAGTTGAGGCAACCAAACCTTCTACTG
 CTGTTGACATCTCTTATTACAGCAACACCATTCTAGGAGTTCTGAGCTCTCCACTGGAG
 TCCTCTTCTGCGGGTCAGAAATTGCCCTAGATGAATGAGAAAATTATTTTTAAT
 TTAAGTCCTAAATATAGTAAATAAATAATGTTTAGTAAATGATACACTATCTGTGA
 AATAGCCTCACCCCTACATGTGGATAGAAGGAAATGAAAAATAATTGCTTGACATTGTCT
 ATATGGTACTTGTAAAGTCATGCTTAAGTACAAATTCCATGAAAAGCTCACACCTGTAAATC
 CTAGCACTTGGGAGGCTGAGGAGGAAGGATCACTGAGGCCAGAAGTTCGAGACTAGCCTG
 GGCAACATGGAGAAGCCCTGTCTACAAAATACAGAGAGAAAAATCAGCCAGTCATGGTG
 GCATACACCTGTAGTCCCAGCATTGGAGGCTGAGGTGGGAGGATCACTGAGGCCAGGG
 AGGTTGGGCTGCAGTGAGCCATGATCACACCACTGCACTCCAGCCAGGTGACATAGCGAGA
 TCCTGTCTAAAAAAATAAATAATGGAACACAGCAAGTCCTAGGAAGTAGGTTAAA
 ACTAATTCTTAA

FIGURE 186

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 27856, pI: 8.50, NX(S/T): 1
MSTTCQVVAFLLSILGLAGCIAATGMDMWSTQDLYDNPVTSVFQYEGLWRSCVRQSSGFTE
CRPYFTILGLPAMLQAVRALMIVGIVLGAIGLLVSIFALKCIRIGSMEDSAKANMTLTSGIM
FIVSGLCAIAGVSFANMLVTNFWMSTANMYTGMGGMVQTVQTRYTFGAALFVGWVAGGLTL
IGGVMMCIAACRGLAPEETNYKAVSYHASGHSVAYKPGGFCASTGFGSNTKNKKIYDGGARTE
DEVQSYPSKHDYV
```

Signal peptide:

amino acids 1-23

Transmembrane domains:

amino acids 81-100, 121-141, 173-194

FIGURE 187

GGAAAAACTGTTCTTCTGTGGCACAGAGAACCGTCAAAAGCAGAAGTAGCAGTTCCG
 GAGTCCAGCTGGCTAAAACATCCCAGAGGATA**ATG**CAACCCATGCCTAGAAATCGCTG
 GGCTGTTCTGGTGGTGAATGGTGGCACAGTGGCTGTCACTGTCATGCCTCAGTGG
 AGAGTGTGCCCTCATTGAAAACAACATCGTGGTTTGAAAACCTCTGGGAAGGACTGTG
 GATGAATTGCGTGAGGCAGGCTAACATCAGGATGCAGTGCAAAATCTATGATTCCCTGCTGG
 CTCTTCTCCGGACCTACAGGCAGCCAGAGGACTGATGTGCTGCTCCGTGATGTCCTTC
 TTGGCTTCATGATGCCATCCTGGCATGAAATGCACCAGGTGCACGGGGACAATGAGAA
 GGTGAAGGCTCACATTCTGCTGACGGCTGGAATCATCTCATCACGGCATGGTGGTGC
 TCATCCCTGTGAGCTGGGTGCCAATGCCATCATCAGAGATTCTATAACTCAATAGTGAAT
 GTGCCCAAAACGTGAGCTGGAGAACGCTCTACTTAGGATGGACCACGGCACTGGTGC
 GATTGTTGGAGGAGCTGTTCTGCTGCGTTTTGCAACGAAAAGAGCAGTAGCTACA
 GATACTCGATACTTCCCATCGCACAAACCAAAAAAGTTATCACACCGGAAAGAAGTCACCG
 AGCGTCTACTCCAGAAGTCAGTATGTG**TAG**TTGTATGTTTTAACTTACTATAAAGC
 CATGCAAATGACAAAAATCTATATTACTTCTCAAAATGGACCCAAAGAAACTTGATTAA
 CTGTTCTTAACTGCCTAATCTAATTACAGGAACTGTGCATCAGCTATTTATGATTCTATAA
 GCTATTCAGCAGAATGAGATATTAAACCAATGCTTGATTGTTCTAGAAAGTATAGTAAT
 TTGTTCTAAGGTGGTCAAGCATCTACTCTTTATCATTACTTCAAAATGACATTGCT
 AAAGACTGCATTATTTACTACTGTAATTCTCCACGACATAGCATTATGTACATAGATGAG
 TGTAACATTATCTCACATAGAGACATGCTTATGGTTATTAAAATGAAATGCCAG
 TCCATTACACTGAATAATAGAACTCAACTATTGCTTTCAGGGAAATCATGGATAGGGTTG
 AAGAAGGTTACTATTAATTGTTAAAACAGCTAGGGATTATGCTCCATTATAATGA
 AGATTAATGAAGGCTTAATCAGCATTGTAAGGAAATTGAATGGCTTCTGATATGCTG
 TTTTTAGCCTAGGAGTTAGAAATCCTAACCTCTTATCCTCTCCAGAGGCTTTTT
 TTCTTGTGTATTAATTAACATTTAAAACGCAGATATTGTCAGGCTTGTCAAGGGCTTGCATTCA
 AACTGCTTCCAGGGCTACTCAGAAGAAAGATAAAAGTGTGATCTAAGAAAAGTGTGATG
 GTTTAGGAAAGTGAAAATATTTGTTTGATTGAAGAAGAATGATGCATTGACAA
 GAAATCATATATGTATGGATATTTAATAAGTATTGAGTACAGACTTGAGGTTTCATC
 AATATAAATAAAAGAGCAGAAAATATGCTTGGTTTCATTGCTTACCAAAAAACAACA
 ACAAAAAAAAGTTGCTTGGAGAACCTCACCTGCTCCTATGTTGGTACCTGAGTCAGGAAATTG
 TCATTTTGTCTGTGAAAATAATTCTTCTGTTATTCAAATTGATGAAACTGACAATCCAATTGA
 AAGTTGTCGACGTCTGTCTAGCTTAAATGAATGTGTTCTATTGCTTATACATTATA
 TTAATAAATTGTACATTTCTAATT

FIGURE 188

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73735
><subunit 1 of 1, 225 aa, 1 stop
><MW: 24845, pI: 9.07, NX(S/T): 0
MATHALEIAGLFLGGVGMVGTVAVTVMPQWRVSAFIENNIVVFENFWEGLWMNCVRQANIRM
QCKIYDSLLALSPDLQAARGLMCAASVMSFLAFMAILGMKCTRCTGDNEKVKAHILLTAGI
IFIITGMVVLIPVSWANAIIRDFYNSIVNVAQKRELGEALYLGWTTALVLIVGGALFCCVF
CCNEKSSSYRYSIPSHRTTQKSYHTGKKSPSVYSRSQYV
```

Signal peptide:

amino acids 1-17

Transmembrane domains:

amino acids 82-101, 118-145, 164-188

FIGURE 189

TCGCC**ATG**GCCTCTGCCCGAATGCAGATCCTGGGAGTCGTCTGACACTGCTGGGCTGGGTG
 AATGGCCTGGTCTCCTGTGCCCTGCCCATGTGGAAAGGTGACCGCTTCATCGAACAGCAT
 CGTGGTGGCCCAGGTGGTGTGGAGGGCCTGTGGATGTCCTGCGTGGTGCAGAGCACCGGCC
 AGATGCAGTGCAAGGTGTACGACTCACTGCTGGCGTGCCACAGGACCTGCAGGCTGCACGT
 GCCCTCTGTGTCATGCCCTCCTGTGGCCCTGTTGGCTTGCTGGTCTACCTGCTGGGC
 CAAGTGTACCACCTGTGTGGAGGAGAAGGATTCCAAGGCCCGCTGGTGCACCTCTGGGA
 TTGTCTTGTCATCTCAGGGGCCTGACGCTAATCCCCGTGTGCTGGACGGCGATGCCATC
 ATCCGGGACTTCTATAACCCCCCTGGTGGCTGAGGCCAAAAGCAGGGAGCTGGGGCCTCCCT
 CTACTTGGGCTGGCGGCCTCAGGCCTTGTGCTGGTGGGGTTGCTGTGCTGCACTT
 GCCCCTGGGGGGTCCCAGGGCCCAAGCCATTACATGGCCGCTACTAACATCTGCCCT
 GCCATCTCTGGGGGCCCTGTAGTACCCATCCAAGAATTACGTC**TGA**CGTGGAGGGGAATG
 GGGGCTCCGCTGGCGCTAGGCCATCCAGAAGTGGCAGTGCCAACAGCTTGGATGGTT
 CGTACCTTTGTTCTGCCTCCTGCTATTGACTGAGGATATTAAAATTCACTT
 GAAAAGTGGAGCCAAGGTGTTGACTCAGACTCTCACCTAGGCTCTGCTGTTCTCACCTGG
 ATGATGGAGCCAAGAGGGATGCTTGAGATTCTGGATCTGACATGCCATCTAGAACGC
 CAGTCAAGCTATGGAACTAATGCCAGGGCTGCTGCTGGCTTGCACAAAGACAGAC
 TGTCCTCAAGAGTTCTGCTGCTGCTGGGGCTGGCTCCCTAGATGTCAGTGACAGCTG
 CCCCATCCTACTCAGGTCTCTGGAGCTCCTCTCTCACCCCTGGAAAAACAAATCATCTG
 TTAACAAAGGACTGCCACCTCCGGAACCTGACCTCTGTTCTCCGTCCTGATAAGACG
 TCCACCCCCCAGGGCCAGGTCCCAGCTATGTAGACCCCCGCCACCTCAAACACTGCACC
 CTTCTGCCCTGCCCTCGTCTCACCCCTTACACTCACATTATCAAATAAGCATG
 TTTTGTAGTGCA

FIGURE 190

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73736
><subunit 1 of 1, 220 aa, 1 stop
><MW: 23292, pI: 8.43, NX(S/T): 0
MASAGMQILGVVLTLLGWVNGLVSCALPMWKVTAFIGNSIIVVAQVVWEGLWMSCVVQSTGQM
QCKVYDSLLALPQDLQAARALCVIALLVALFGLLVYLAGAKCTTCVEEKDSKARLVLTSIV
FVISGVTLIIPVCWTAHAIIRDFYNPLVAEAQKRELGASLYLGWAASGLLLLGGGLLCTCP
SGGSQGPSPHYMARYSTSAPAISRGPSEYPTKNYV
```

Transmembrane domains:

amino acids 8-30 (type II), 82-102, 121-140, 166-186

FIGURE 191

GCCAAGGAGAACATCATCAAAGACTCTAGACTCAAAAGGCTCCACGTTCTACATCTTG
 AGCATCTTCTACCACTCCGAATTGAACCAGTCTCAAAGTAAAGGCAATGGCATTATCCC
 TTGCAAATTGCTGGCTGGTTCTGGGTCCTGGCATGGTGGGGACTCTGCCACAACCCT
 TCTGCCTCAGTGGTGGAGTATCAGCTTGTTGGCAGCAACATTATTGTCTTGAGAGGGCTC
 TGGGAAGGGCTCTGG**ATG**AATTGCATCCGACAAGCCAGGGTCCGGTTGCAATGCAAGTTCTA
 TAGCTCCTTGTGGCTCTCCGCCTGCCCTGGAAACAGCCCCGGCCCTCATGTGTGGCTG
 TTGCTCTCTCCTTGATGCCCTGCTTATTGGCATCTGTGGCATGAAGCAGGTCCAGTGCACA
 GGCTCTAACGAGAGGGCCAAGCATACTTCTGGGAACCTCAGGAGTCCTCTTCATCCTGAC
 GGGTATCTCGTTCTGATTCCGGTGAGCTGGACAGCCAATATAATCATCAGAGATTCTACA
 ACCCAGCCATCCACATAGGTCAAGAACGAGAGCTGGAGCAGCACCTTCTGGCTGGCA
 AGCGCTGCTGTCCTCTCATTGGAGGGGGCTGCTTGTGGATTGGCTGCAACAGAAA
 GAAGCAAGGGTACAGATATCCAGTGCCTGGCTACCGTGTGCCACACACAGATAAGCGAAGAA
 ATACGACAATGCTTAGTAAGACCTCCACCAGTTATGTC**TAA**TGCCTCCTTGGCTCCAAGT
 ATGGACTATGGTCAATGTTTTATAAAGTCCTGCTAGAAACTGTAAGTATGTGAGGCAGGA
 . GAACTTGCTTATGTCTAGATTACATTGATACGAAAGTTCAATTGTTACTGGTGGTAGG
 AATGAAAATGACTTACTGGACATTCTGACTTCAGGTGTATTAAATGCATTGACTATTGTTG
 GACCCAATCGCTGCTCCAATTTCATATTCTAAATTCAAGTATACCCATAATCATTAGCAAG
 TGTACAATGATGGACTACTTATTACTTTGACCATCATGTATTATCTGATAAGAATCTAAA
 GTTGAAATTGATATTCTATAACAATAAACATACCTATTCTA

FIGURE 192

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73737
><subunit 1 of 1, 173 aa, 1 stop
><MW: 18938, pI: 9.99, NX(S/T): 1
MNCIRQARVRLQCKFYSSLLALPPALETARALMCVAVALSLIALLIGICGMKQVQCTGSNER
AKAYLLGTSGVLFILTGIFVLIPIPVSWTANIIIRDYNPALIHIGQKRELGAALFLGWASAABL
FIGGGILLCGFCCCNRKKQGYRYPVPGYRVPHTDKRRNTTMLSKTSTSYY
```

Important features of the protein:

Transmembrane domains:

amino acids 31-51, 71-90, 112-133

N-glycosylation site.

amino acids 161-164

FIGURE 193

AGTGACAATCTCAGAGCAGCTTCTACACCACAGCCATTCCAGCATGAAGATCACTGGGGT
CTCCTTCTGCTCTGTACAGTGGCTATTTCTGTAGCAGCTCAGAAGCTGCTAGTCTGTCTCC
AAAAAAAGTGGACTGCAGCATTACAAGAAGTATCCAGTGGTGGCCATCCCCTGCCCATCA
CATACCTACCAGTTGTGGTTCTGACTACATCACCTATGGAATGAATGTCACTTGTGTACC
GAGAGCTTGAAAAGTAATGGAAGAGTTCAGTTCTCACGATGGAAGTTGCTAAATTCTCCA
TGGACATAGAGAGAAAGGAATGATATTCTCATCATCATCTTCACTCATCCCAGGCTCTGACTG
AGTTTCTTCAGTTTACTGATGTTCTGGGTGGGGACAGAGCCAGATTCAAGTAATCTTG
ACTGAATGGAGAAAGTTCTGTGCTACCCCTACAAACCCATGCCTCACTGACAGACCAGCAT
TTTTTTTTAACACGTCAATAAAAAATAATCTCCCAGA

FIGURE 194

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73739
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9232, pI: 7.94, NX(S/T): 0
MKITGGLLLLCTVYYFCSSSEAASLSPKKVDCSIYKKYPVVAIPCPITYLPVCGSDYITYGN
ECHLCTESLKSNGRVQFLHDGSC
```

Signal peptide:

amino acids 1-19

FIGURE 195

CCCGCGCCCCGGTTCTCCCTCGCAGCACCTCGAAGTGCGCCCTCGCCCTCCTGCTCGCGCCC
CGCCGCC**ATG**GCTGCCTCCCCCGCGGCCCTGCTGTCTGCCCTGACCGGGCTGGCGCTGC
TCCTGCTCCTGTGCTGGGGCCCAGGTGGCATAAGTGGAAATAAACTCAAGCTGATGCTCAA
AAACGAGAAGCACCTGTTCCAACTAAGACTAAAGTGGCCGTTGATGAGAATAAGCAAAGA
ATTCCCTGGCAGCCTGAAGGCCAGAAGCGGCAGCTGTGGGACCGGACTCGGCCGAGGTGC
AGCAGTGGTACCAGCAGTTCTACATGGCTTGATGAAGCGAAATTGAAGATGACATC
ACCTATTGGCTTAACAGAGATCGAAATGGACATGAATACTATGGCGATTACTACCAACGTCA
CTATGATGAAGACTCTGCAATTGGTCCCCGGAGCCCTACGGCTTAGGCATGGAGCCAGCG
TCAACTACGATGACTAC**TAA**CCATGACTTGCACACGCTGTACAAGAAGCAAATAGCGATT
TCTTCATGTATCTCTTAATGCCTTACACTACTTGGTTCTGATTTGCTCTATTCAGCAGAT
CTTTCTACCTACTTGTGTGATAAAAAGAAGAGTTAAAACAACACATGTAAATGCCTT
TGATATTCATGGGAATGCCTCTCATTTAAAAATAGAAATAAGCATTGTTAAAAGA

FIGURE 196

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73742
><subunit 1 of 1, 148 aa, 1 stop
><MW: 17183, pI: 8.77, NX(S/T): 0
MAASPARPAVLALTGLALLLLCWGP GGISGNKLKMLQKREAPVPTKTVAVDENAKEFL
GSLKRQKRQLWDRTRPEVQQWYQQFLYMGFDEAKFEDDITYWLNRDRNGHEY YGDYYQRHYD
EDSAIGPRSPYGF RGASVNYDDY
```

Signal peptide:

amino acids 1-30

bio 4410 bio 4410 bio 4410 bio 4410

FIGURE 197

CGGCTCGAGCCGCCGGAAAGTGCCCGAGGGGCCGCGATGGAGCTGGGGAGCCGGCGCTC
 GGTAGCGCGGGCAAGGCAGGCATGACCTGATTGAAGGGTGGGTGATGAGGTGAC
 CGTCCTTTCTCGGTGCTTGCCTGCCTCTGGTGCCTGGCCCTTGCCCTGGTCTCAACGCACA
 CCGCTGAGGGCGGGACCCACTGCCCGTCAGGGACCCAACGCCATCCCAGCCCAGC
 GCAGCCATGGCAGCTACCGACAGCATGAGAGGGAGGCCAGGGCAGAGACCCCCAGCCT
 GAGACACAGAGGTCAAGCTGCACAGCCAGAGCCCAGCACGGGTTCACAGCAACACGCCAG
 CCCCGGACTCCCCGAGGCCCTCGTGCCTACGGCTGAAATTCTCAATGATTAGCAGAGCAG
 GTGGCCAGGGCTGGCCCCACGACACCATTGGCTCCTGAAAAGGACCCAGTTCCCAGCG
 GGAACACAGGTGCGACTCATCTACCAAGGGCAGCTGCTAGGCGACGACACCCAGACCCCTGG
 GCAGCCTCACCTCCCTCCAACTGCCTCTCCACTGCCACGTGTCACGAGAGTCGGTCCC
 CCAAATCCCCCTGCCGCCGGGTCCGAGGCCGGCCCTCCGGCTGGAAATCGGCAGCCT
 GCTGCTGCCCTGCTGCTCCTGCTGTTGCTGCTGCTCTGGTACTGCCAGATCCAGTACCGC
 CCTTCTTCCCCCTGACCGCCACTCTGGCCTGGCCGGCTTACCCCTGCTCCTCAGTCTCCTG
 GCCTTGCCATGTACCGCCTAGGCCTCCGCCGGCGCTGGCAGCGTCGCCGGCCCTCC
 GGACCTTGCTCCCCGCCGCCGGAGCTGCTGCCTGCCAGGCCGCCCTCCGGCCTG
 CCTCTTCCCCGCTGCCCTGGAGCCCAGCCCTGCCGCCAGAGGAATCCGGACTGGCGGAGG
 CCCGCCCTGCGACCGCCGGGCTGGGGCACCTCCGGGCTGCTGAACCTCAGCCGCA
 CTGGGAGTGGGCTCCTGGGTGGGCATCTGCTGCTGCCCTGCCGGGGCAGAGCCG
 GGCGCCCCGGGGCCGTCTAGTGTCTGCCGGAGGACCCAGCCGCCCTCCAATCCCTGAC
 AGCTCCTTGGGCTGAGTTGGGACGCCAGGTGGTGGAGGCTGGTGAAGGGAGCGGGAG
 GGGCAGAGGAGTTCCCCGAAACCGTGCAGATTAAAGTAACGTGAAGTTAAAAAAA
 AAAAAAAA

FIGURE 198

MTLIEVGDEVTVLFSVLACLLVLALAWVSTHTAEGGDPLPQPSGTPTPSQPSAAMAATDSM
RGEAPGAETPSLRHRGQAAQPEPSTGFTATPPAPDSPQEPLVRLKFLNDSEQVARAWPHDT
IGSLKRTQFPGREQQVRLIYQGQQLLGDDTQLGSLHLPPNCVLHCHVSTRVGPPNPPCPPGS
EPGPSGLEIGSLLLPLLWYCQIQYRPFFPLTATLGLAGFTLLSLLAFAMYRP

Signal peptide:

amino acids 1-31

Transmembrane domain:

amino acids 195-217

FIGURE 199

GAGATTGGAAACAGCCAGGTTGGAGCAGTGAGTGAGTAAGGAAACCTGGCTGCCCTCTCCAG
 ATTCCCCAGGCCTCTCAGAGAAGATCAGCAGAAAGTCTGCAAGACCCTAACGAACCATCAGCCC
 TCAGCTGCACCTCCTCCCTCCAAGG**ATG**ACAAAGGCGCTACTCATCTATTGGTCAGCAGC
 TTTCTGCCCTAAATCAGGCCAGCCTCATCAGTCGCTGTGACTTGGCCCAGGTGCTGCAGCT
 GGAGGACTTGGATGGGTTTGAGGGTTACTCCCTGAGTGACTGGCTGTGCCTGGCTTTGTGG
 AAAGCAAGTTCAACATATCAAAGATAAAATGAAAATGCGGATGGAAGCTTGACTATGGCCTC
 TTCCAGATCAACAGCCACTACTGGTGCAACGATTATAAGAGTTACTCGGAAACCTTGCCTA
 CGTAGACTGTCAAGATCTGCTGAATCCCAACCTTCTTGCAGGCATCCACTGCGAAAAAGGA
 TTGTGTCCGGAGCACGGGGATGAACAACTGGGTAGAATGGAGGGTTGCACTGTTCAGGCCGG
 CCACTCTCCTACTGGCTGACAGGATGCCGCTGAGA**TGA**AAACAGGGTGCAGGTGCACCGTGG
 AGTCATTCCAAGACTCCTGTCCTCACTCAGGGATTCTTCATTCTTCTCCTACTGCCTCCA
 CTTCATGTTATTTCTCCCTCCATTACAACACTAAAGCTGACCAGAGCCCCAGGAATAAA
 TGGTTTCTTGGCTTCCTCCTACTCCCCTGGACCCAGTCCCTGGTCTGTCTGTTAT
 TTGTAACGTAGGGACCACAATAAAGAAATCTTATATTATCG

FIGURE 200

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73746
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16896, pI: 6.05, NX(S/T): 1
MTKALLIYLVSSFLALNQASLISRCDLAQVLQLEDLDGFEGYSLSDWLCLAFVESKFNISKI
NENADGSFDYGLFQINSHWCNDYKSYSLENLCHVDCQDLLNPNLLAGIHCAKRVSGARGMN
NWVEWRLHCSGRPLSYWLTGCRLR
```

Signal peptide:

amino acids 1-18

A C D E F G H I K M L V P Q R S T W Y N

FIGURE 201

TCTGACCTGACTGGAAAGCGTCAAAGAGGGACGGCTGTAGCCCTGCTTGACTGAGAACCCA
CCAGCTCATCCCAGACACCTCATAGAACCTATTATACAAGGGGAAAGAACACCTGAG
CAAAATGGAATCATTATTTTCCAAAGGAGAAAACCGGGTAAAGGGAGGGAAAGCAATT
AATTGAAAGTCCCTGTGAATGGGCTTCAGAAGGCAATTAAAGAAATCCACTCAGAGAGGAC
TTGGGGTGAACACTTGGGCCTGTGGTTCTGATTGTAAGTGGAAAGCAGGTCTGCACACGC
TGTGGCAAATGTCAGGACCAGGTTAAGTGACTGGCAGAAAAACTCCAGGTGGAAACAAGCA
ACCCATGTTCTGCTGCAAGCTGAAGGAGCCTGGAGCGGGAGAAAGCTAACTTGAACATGAC
CTGTTGCATTGGCAAGTTCTAGCAAC**ATG**CTCCTAAGGAAGCGATAACAGGCACAGACCATG
CAGACTCCAGTCCCTCTGCTGCTCCTGATGCTGGATGCGTCCTGATGATGGTGGCGATGT
TGCACCCCTCCCCACACACCCCTGCACCAGACTGTCACAGCCCAAGGCCAGCAAGCACAGCCCT
GAAGCCAGGTACCGCTGGACTTGGGAATCCCAGGATTGGTACTGGAAGCTGAGGATGA
GGGTGAAGAGTACAGCCCTCTGGAGGGCTGCCACCCCTTATCTCACTGCGGGAGGATCAGC
TGCTGGTGGCGTGGCCTTACCCAGGCCAGAAGGAACCAGGCCAGGGCAGGAGAGGTGGG
AGCTACCGCCTCATCAAGCAGCCAAGGAGGCAGGATAAGGAAGCCCCAAAGAGGGACTGGGG
GGCTGATGAGGACGGGGAGGTGTCTGAAGAAGAGGAGTTGACCCCGTCAGCCTGGACCCAC
GTGCCCTCCAGGAGGCACTCAGTGCCCGATCCCCCTCCAGAGGGCTTGCCCGAGGTGCGG
CACCCACTGTGTCTGCAGCAGCACCCCTCAGGACAGCCTGCCACAGCCAGCGTCATCCTCTG
TTTCCATGATGAGGCTGGTCACTCTCCTGCGGACTGTACACAGCATCCTGACACAGTGC
CCAGGGCCTCCTGAAGGAGATCATCCTCGTGGACGACCTCAGCCAGCAAGGACAACCTCAAG
TCTGCTCTCAGCGAATATGTGCCAGGCTGGAGGGGGTGAAGTTACTCAGGAGCAACAAGAG
GCTGGGTGCCATCAGGGCCGGATGCTGGGGGCCACCAGGCCACCGGGGATGTGCTCGTCT
TCATGGATGCCACTGCGAGTGCCACCCAGGCTGGCTGGAGCCCCCTCCTCAGCAGAATAGCT
GGTACAGGAGCCAGTGGTATCTCCGGTGTAGATGTGATTGACTGGAAGACTTCCAGTA
TTACCCCTCAAAGGACCTGCAGCGTGGGTGTTGACTGGAAGCTGGATTTCACGGGAAC
CTTGCCAGAGCATGTGAGGAAGGCCCTCAGTCCCCATAAGCCCCATCAGGAGCCCTGTG
GTGCCCGGAGAGGTGGTGGCCATGGACAGACATTACTTCAAAACACTGGAGCGTATGACTC
TCTTATGTCGCTGCGAGGTGGTGAACACTGTCTTCAAGGCCCTGGCTCTGGTG
GCTCTGTTGAAATCCTCCCTGCTCTGGTAGGACACATCTACAAAATCAGGATCCCCAT
TCCCCCTCGACCAGGAGGCCACCCCTGAGGAACAGGGTTCGATTGCTGAGACCTGGCTGG
GTCATTCAAAGAAACCTTCTACAAGCATGCCAGAGGCCCTCTCCTGAGCAAGGCTGAGA
AGCCAGACTGCATGGAACCGCTTGCAGCTGCAAAGGAGACTGGGTTGTCGGACATTCCACTGG
TTCTGGCTAATGTCTACCCCTGAGCTGTACCCATCTGAACCCAGGCCAGTCTCTGGAAA
GCTCCACAACACTGGACTTGGCTCTGCAAGACTGCCAGGCCAGAAGGGGACATCCTGGCT
GTCCCAGGGTGTGGCTCTGCAAGTACAGGCCAGCAACAGTACCTGCAGCACACCAGC
AGGAAGGAGATTCACTTGGCAGCCCACAGCACCTGTGCTTGTCAAGGCCAGGAGCAGGT
GATTCTCAGAACTGCACGGAGGAAGGCCATCCACCCAGCAGCACTGGGACTTCCAGG
AGAATGGGATGATTGTCACATTCTTCTGGAAATGCATGGAAGCTGTGGTCAAGAAAAC
AATAAAGATTGTACCTGCGTGTGTGATGGAAAAGCCGCCAGCAGTGGCGATTGACCA
GATAAATGCTGTGGATGAACGAT**TGA**ATGTCATGTCAGAAGGAAAAGAGAATTGGCCATC
AAAATCCAGCTCCAAGTGAACGTAAGAGCTTATATATTGACCATGAAAGCTGATCCTTGTG
GTGTGCTCCTGTGTTAGGAGAGAAAAAGCTATGAAAGAATATAGGAAGTTCTCCTT
TCACACCTTATTCATTGACTGCTGGCTGCTTA

FIGURE 202

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA73760
 ><subunit 1 of 1, 639 aa, 1 stop
 ><MW: 73063, pI: 6.84, NX(S/T): 2
 MLLRKRYRHRPCRLQFLLLLMLGCVLMMVAMLHPPHHTLHQTVTAQASKHSPEARYRLDFG
 ESQDWVLEAEDEGEEYSPLEGLPFFISLREDQLLVAALPQARRNQSQGRGGSYRLIKQPR
 RQDKEAPKRDWGADEDGEVSEEEELTPFSLDPRGLQEALSARIPLQRALPEVRHPLCLQQHP
 QDSLPTASVILCFHDEAWSTLLRTVHSILDTPRAFLKEIIILVDDLSQQGQLKSALSEYVAR
 LEGVKLLRSNKRLGAIRARMLGATRATGDVLVFMDAHCECHPGWLEPLLSRIAGDRSRVVSP
 VIDVIDWKTFQYYPSKDLQRGVLDWKLDHFWEPLPEHVRKALQSPISPPIRSPVVPGEVVAMD
 RHYFQNTGAYDSLMSLRGGENLELSFKAWLCGGSVEILPCSRVGHIYQNQDSHSPLDQEATL
 RNRVRIAETWLGSFKETFYKHSPEAFSLSKAEPDCMERLQLQRRLGCRTFWFLANVYPEL
 YPSEPRPSFSGKLHNTGLGLCADCQAEGDILGCPMVLAPCSDSRQQYLQHTSRKEIHFGSP
 QHLCFAVRQEQQVILQNCTEEGLAIHQHQHWDQENGIVHILSGKCMEAVVQENNKDLYLRPC
 DGKARQQWRFDQINAVDER

Signal peptide:

amino acids 1-28

FIGURE 203

CGCCAAGCATGCAGTAAAGGCTGAAAATCTGGGTACAGCTGAGGAAGACCTCAGACATGGA
 GTCCAGGATGTGCCCTGCGCTGCTGCTGTCACCTCCCTCTGGCCACTGCTGTTGC
 TGCCCCCTCCCACCGCCTGCTCAGGGCTCTCATCCTCCCTCGAACCCCCACCAGCCCCAGCC
 CGCCCCCCCCTGTGCCAGGGAGGCCCTCGGCCCCACGTATGTGCGTGTGGGAGCGAGC
 ACCTCCACCAAGCCGATCTCCTCGGGTCCAAGATCACGTGGCAAGTCCTGCCTGGCACTG
 CACCCCCAGCCACCCCATCAGGCTTGAGGAGGGGCCCTCATCCAATACCCCTGGGCT
 ATCGTGTGGGGTCCCACCGTGTCTCGAGAGGATGGAGGGACCCAACTCTGCCAATCCCGG
 ATTTCTGGACTATGGTTTGAGCCCTCATGGGCTCGAACCCCCACACCCCAACTCAGACT
 CCATGCGAGGTGATGGAGATGGGTTATCCTGGAGAGGCACCTGCCACCCCTGCGGCCATT
 CTGTTGGGGGCCGTGGGAAGGTGTGGACCCCCAGCTATGTCACAATTACCATCTCCAT
 CATCATTGTTCTCGTGGCCACTGGCATCATCTCAAGTTCTGCTGGGACCGCAGCCAGAAC
 GACGCAGACCCCTCAGGGCAGCAAGGTGCCCTGAGGCAGGAGGAGGCCAGCAGCCACTGACA
 GACCTGTCCCCGGCTGGAGTCACTGTGCTGGGGCCTCGGGGACTCACCTACCCCCACCC
 TGACCATGAGGAGCCCCGAGGGGACCCCGCTGGGATGCCCAAGGGGCTCCAG
 CCTTCCAGTTGAACCGGTGAGGGCAGGGCAATGGGATGGGAGGGCAAAGAGGGAAAGGCAAC
 TTAGGTCTTCAGAGCTGGGTGGGGTGCCTCTGGATGGTAGTGAGGAGGCAGGCAGCAG
 CTCCCACAGCCCTGGCCCTCCCAAGGGGCTGGACAGCTCCTCTGGGAGGCACCCCTC
 CTTCTCCAGTCTCTCAGGATCTGTGTCCTATTCTCTGCTGCCATAACTCCAACCTGCC
 TCTTGGTTTTCTCATGCCACCTGTCTAAGACAACCTGCCCCTCTAACCTGATTCCC
 CCTCTTGTCTTGAACCTCCCTCTATTCTGCCCTACCCCTGGTTCTGACTGTGCCCTT
 TCCCTCTCCTCTCAGGATTCCCTGGTAATCTGTGATGCCCAATGTTGGGTGCAGCC
 AAGCAGGAGGCCAAGGGGCCGGCACAGCCCCATCCACTGAGGGTGGGCAGCTGTGGGA
 GCTGGGCCACAGGGCTCCTGGCTCCTGCCCTTGACACACCACCGAACACTCCCCAGCC
 CCACGGCAATCTATCTGCTGCCCTCTGCAGGTGGGGCTCACATATCTGTGACTTCG
 GGTCCCTGTCCCCACCCCTGTGCACTCACATGAAAGCCTGACACTCACCTCACCTCAC
 AGGCCATTGACACGCTCCTGCACCCCTCTCCGTCATACCGCTCCGCTCAGCTGACTCT
 CATGTTCTCTGCTCACATTGCACTCTCTCCACATTCTGTGCTCAGCTCACTCAG
 TGGTCAGCGTTCTGCACACTTACCTCATGTCGTTCCGGCTGATGTTGTGGTGG
 TGTGCGGCGTGCCTACTCTCTCCCTCATGAACACCCACCCACCTCGTTCCGAGCCCCCTGC
 GTGCTGCTCCAGAGGTGGGTGGGAGGTGAGCTGGGGCTCCTGGGCCCTCATCGGTATGG
 TCTCGTCCCATTCCACACCATTGTTCTGTCTCCCTACTCCAAGGATGCCGGCA
 TCACCCCTGAGGGCTCCCCCTGGGAATGGGGTAGTGAGGCCAGACTCACCCCCAGGCCA
 CTGCTAAAATCTGTTCTGACAGATGGGTTTGGGAGTCGCCTGTCAGTACATGAGAA
 AGGGACTCCCATTGCCCTCCCTCTCCTACAGTCCCTTGTCTGTCTGCTGGCTG
 TCTGTGTGTGCCCCCTCTGGACTTCAGAGCCCCCTGAGCCAGTCCTCCCTCCAGCCT
 CCCTTGGGCCTCCCTAACCTCCACCTAGGCTGCCAGGGACCGGAGTCAGCTGGTTCAAGGCC
 ATCGGGAGCTGCCTCCAAGTCTACCCCTCCCTCCGGACTCCCTCTGTCCCCCTCCTT
 CCTCCCTCTCTCACTGGTTTCCACCTCCCTCCCTTCCCTGGCTCCTAGGCT
 CTTCCCTCTCACTGGTTTCCACCTCCCTCCCTTCCCTGGCTCCTAGGCT
 GTGATATATATTTGTATTATCTCTTCTTGTGGTGTGATCATCTGAATTACTGTG
 GGATGTAAGTTCAAAATTCAAATAAGCCTTGCAAGATAA

FIGURE 204

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKGEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECSGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIELPK
```

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217

FIGURE 205

GTAAACCAGCGCAGTCCTCCGTGCGTCCC GCCGCGCTGCCCTCACTCCC GCCAGG**ATGG**
CAT CCT GTCTGGCCCTGCGCATGGCGCTGCTGGTCTCCGGGTCTGGCCCTGCGGTG
CTCACAGACGATGTTCCACAGGGAGCCGTGCCACGCTGTGGAACGAGCCGGCGAGCTGCC
GTCGGGAGAAGGCCCCGTGGAGAGCACCAGCCCCGGCCGGAGGCCGTGGACACCGGTCCCC
CAGCCCCCACCGTCGCCAGGACCCGAGGA CAGCACCGCGCAGGAGCGGCTGGACCAGGGC
GGCGGGTCGCTGGGCCCGCGCTATCGCGGCCATCGTATGCCGCCCTGCTGGCCACCTG
CGTGGTGCTGGCGCTCGTGGTCGCGCTGAGAAAGTTTCTGCCTCC**TGA**AGCGAATAAA
GGGGCCGCGCCCGGCCGCGCGACTCGGCAAAAAAAAAAAAAAA

FIGURE 206

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76398
><subunit 1 of 1, 121 aa, 1 stop
><MW: 12073, pI: 4.11, NX(S/T): 0
MASCLALRMALLLVSGVLAPAVLTDDVPQEPVPTLWNEPAELPSGEGPVESTSPGREPVDTG
PPAPTVAPGPEDSTAQERLDQGGGSLGPGAIAAIVIAALLATCVVLALVVVALRKFSAS
```

Important features of the protein:

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 91-110

Glycosaminoglycan attachment site.

amino acids 44-47

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 116-119

N-myristoylation site.

amino acids 91-96

FIGURE 207

GGCGTTGGTGGCTGCGGGCTGAAGGGTGTGGCGAGCAGCGTCGGTGGCTGGCCGGCG
 CGGGCCGGGACGGGCATGGCCCTGCTGCTGTGCCTGGTGTGCCTGACGGCGGCGCTGGCCA
 CGGCTGTCTGCACTGCCACAGCAACTTCTCCAAGAAGTTCTCCTTCTACCGCCACCATGTGA
 ACTTCAAGTCCTGGTGGGTGGCGACATCCCCGTGTCAGGGCGCTGCTCACCGACTGGAGC
 GACGACACGATGAAGGAGCTGCACCTGGCATCCCCGCCAAGATCACCCGGAGAACGCTGGA
 CCAAGTGGCGACAGCAGTGTACCAAGATGATGGATCAGCTGTACCAAGGGAAAGATGTACTTCC
 CCGGGTATTCCCCAACGAGCTGCGAAACATCTTCCGGAGCAGGTGCACCTCATCCAGAAC
 GCCATCATCGAAAGGCACCTGGCACCAGGCAGCTGGGAGGGAGGGCAGCTCTCCAGGGAGGG
 ACCCAGCCTAGCACCTGAAGGATCAATGCCATCCCCGGGGACCTCCCCTAAGTAGCCC
 CCAGAGGCGCTGGAGTGTGCCCCCCTCCGGGACCCCTCCGGGCATGGACACACATACATGAAAACCAGGCC
 GTCAACCTGGGGACCCCTCCGGGCATGGACACACATACATGAAAACCAGGCC
 CGACTGTCAGCACCGCTGTGGCATCTTCAGTACGAGACCATCTCCTGCAACAACACTGCACAG
 ACTCGCACGTCGCCTGCTTGCTATAACTGCGAGTAGGGCTCAGGCATCACACCCACCGT
 GCCAGGGCCCTACTGTCCCTGGGTCCCAGGCTCTCCTGGAGGGGCTCCCCGCTTCCAC
 CTGGCTGTCACTGGGTAGGGCGGGGCCGTGGTTCAAGGGCGCACCACCTCCAAGCCTGTGT
 CCCACAGGTCTCGCGCAGTGGAAAGTCAGCTGTCCAGGGCCTCTGAACACTACATAAAAC
 TGGCACAAGTAAGTCCCCCTCAAACCAACACAGGCAGTGTGTATGTGAGCACCTCGT
 GGTGAGTATGTGTGGGGCACAGGCTGGCTCCCTCAGCTCCACGTCTAGAGGGCTCCGA
 GGAGGTGGAACCTCAACCCAGCTCTGCGCAGGAGGGGGCTGCAGTCCTTCTCCCTCAAAG
 GTCTCCGACCCCTCAGCTGGAGGGGGCATCTTCTAAAGGGTCCCCATAGGGTCTGGTCC
 ACCCCATCCCAGGTCTGGTCAGAGCCTGGAGGGTCCCTACGATGGTTAGGGGTGCC
 ATGGAGGGGCTGACTGCCACATTGCCTTCAGACAGGACACGAGCATGAGGTAAGGCC
 CCTGACCTGGACTTCAGGGGGAGGGGTAAGGGAGAGAGGAGGGGGCTAGGGGTCC
 AGATCAGTGGGGCACTGCAGGTGGGCTCTCCCTACCTGGACACCTGCTGGATGTCAC
 CTCTGCAACCACACCATGTGGTGGTTCATGAACAGACACCAGCTCCTCTGCCTCTC
 CCTGGACACACAGAGCCACCCGGCTTGTGAGTGACCCAGAGAACGGAGGC
 AGGGGTCTCGTAAGCCAACACCAGCGTGGCGCGCTGCACACCCCTCGGACATCCCAGGC
 ACGAGGGTGTGAGTGTGGCACACATAGGACCAACACGTCAGCTGGAGGGAGAGGC
 GGGGCCAGGGAGGGAGGCAGGGGTGGGGACATGGAGAGCTGAGGCAGGC
 CCTGGACCTGGTATGCCAGCCTTAAGGTGTCTGGAGCCCCACACTTGGCCAACCTGACCT
 TGGAAGATGCTGCTGAGTGTCTCAAGCAGCACTGACAGCAGCTGGCCTGCCAGGGCAAC
 GTGGGGCGGAGACTCAGCTGGACAGCCCCCTGCCTGTCACTCTGGAGCTGGCTGCTGC
 CTCAGGACCCCTCTCCGACCCGGACAGAGCTGAGCTGGCCAGGGCAGGAGGGCGGGAGG
 GAGGGAATGGGGTGGCTGTGCGCAGCATCAGCGCCTGGGCAGGTCCGCAGAGCTGC
 TGTGATTAAAGTCCCTGATGTTCTC

FIGURE 208

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76399
><subunit 1 of 1, 157 aa, 1 stop
><MW: 17681, pI: 7.65, NX(S/T): 1
MALLLCLVCLTAALAHGCLHCHSNFSKKFSFYRHHVNFKSWWVGDI PVSGALLTDWSDDTMK
ELHLAIPIAKITREKLDQVATAVYQMMMDQLYQGKMYFPGYFPNELRNIFREQVHLIQNATIER
HLAPGSWGGGQLSREGPSLAPEGSMPSPRGDLP
```

Signal peptide:

amino acids 1-15

卷之三

FIGURE 209

AGCAGGAGCAGGAGAGGGACA**ATG**GAAGCTGCCCGTCCAGGTTCATGTTCCCTTATTCT
 CCTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTG
 GTGCTGCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCAATTGCTGCC
 ACTGAGGTGGCTGTCATAGGCTTCTCAGGATTAGAAATACCAAGCAGTGCCCATACTCCA
 TAGCATGGTGCAAAAATTCCCAGGCGTGTCAATTGGGATCAGCACTGATTCTGAGGTTCTGA
 CACACTACAAACATCACTGGAACACCATCTGCCTCTTCGCCTGGTAGACAATGAACAACTG
 AATTAGAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGGCCATTGAGAT
 CAACAGCCTCCACATGGTACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCG
 TAATTCAAGATTCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATG
 CACAGATACCAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTATTCTGGTGGACAG
 TGGTATGAAAGAAAATGGGAAGGTGATATCATTTCAAACTAAAGGAGTCTCAACTGCCAG
 CTTGGCAATTACCAAGACTCTAGATGACGAGTGGGATACACTGCCACAGCAGAAGTTCC
 GTAGAGCATGTGCAAAACTTTGTGATGGATTCTAAGTGGAAAATTGTTGAAAGAAAATCG
 TGAATCAGAAGGAAAGACTCCAAAGGTGGAAC**TGA**CTTCTCCTGGAACTACATATGCC
 AAGTATCTACTTATGCAAAGTAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAG
 GATCACTAGGCCTGCCAACACACACACACACAGCAGCTCATTCCCTGTCTTAAATCTGTTCTC
 ACACACGCGCACACACACACACACAGAGCTCATTCCCTGTCTTAAATCTGTTCTC
 TTCTCCTTCTTAAATTCATATCCTCACTCCATCCAAATTCCCTTATCGTGCATT
 CATACTCTGTAAGCCCACCTGTAACACACACTAGATCAAGGCTTAAGAGACTCACTGTGATG
 CCTCTATGAAAGAGAGGCATTCTAGAGAAAGATTGTTCCAATTGTCATTTAATATCAAGT
 TTGTATACTGCACATGACTTACACACAACATAGTCCCTGCTTTAAGGTTACCTAAGGGT
 TGAAACTCTACCTTCTTCATAAGCACATGTCCGTCTGACTCAGGATAAAAACCAAAGG
 ATGGTTTAAACACCTTGTGAAATTGTCTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTC
 CCTGAACTCAGCAGAAATAGACCATGTGAAAACCTCCATGCTGGTTAGCATCTCCAACCTCC
 TATGTAATCAACAACCTGCATAATAAAAAGGCAATCATGTTATA

FIGURE 210

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401
><subunit 1 of 1, 273 aa, 1 stop
><MW: 30480, pI: 4.60, NX(S/T): 1
MEAAPSRRMFLLFLLTCELAAEVAEVEKSSDGPAGAAQEPTWLTDVPAAMEFIAATEVAVIG
FFQDLEIPAVPILHSMVQKFPGVSGFISTDSEVLTHYNITGNTICLFRLVDNEQLNLEDEDI
ESIDATKLSRFIEINSLHMVTEYNPVTIVIGLFNSVIQIHLLLIMNKASPEYEENMHRYQKAA
KLFQGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDEWDTLPTAEVSVEHVQNF
CDGFLSGKLLKENRESEGKTPKVEL
```

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

FIGURE 211

GGAGAGCCGGCTGGGACCGGAGTGGGGAGCGCGCGGTGGAGGTGCCACCCGGCGCGGGTG
 GCGGAGAGATCAGAAGCCTCTTCCCCAAGCCGAGCCAACCTCAGCAGGGGACCCGGGCTCAGG
 GACGCGGGCGGGCGGGCGACTGCAGTGGCTGGACG**ATGG**CAGCGTCCGCCGGAGCCGG
 GCGGTGATTGCAGCCCCAGACAGCCGGCGTGGCTGTGGTCGGTGCTGGCGGGCGCTTGG
 GCTCTTGACAGCTGGAGTATCAGCCTGGAAGTATATACGCCAAAAGAAATCTCGTGGCAA
 ATGGTACACAAGGAAAGCTGACCTGCAAGTTCAAGTCTACTAGTACGACTGGCGGGTTGACC
 TCAGTCTCCTGGAGCTCCAGCCAGAGGGGGCGACACTACTGTGTCGTTTCCACTACTC
 CCAAGGGCAAGTGTACCTTGGGAATTATCCACCATTAAAGACAGAACAGCTGGGCTGGAG
 ACCTTGACAAGAAAGATGCATCAATCACATAGAAAATATGCAGTTATACACAATGGCACC
 TATATCTGTGATGTCAAAAACCCCTCTGACATCGTTGTCCAGCCTGGACACATTAGGCTCTA
 TGTCGTAGAAAAAGAGAATTGCGCTGTGTTCCAGTTGGTAGTGGTGGGCATAGTTACTG
 CTGTGGCCTAGGTCTCACTCTGCTCATCAGCATGATTCTGGCTGTCCCTATAGAAGGAAA
 AACTCTAACGGGATTACACTGGCTGCAGTACATCAGAGAGTTGTACCAAGTTAACAGGC
 TCCTCGGAAGTCCCCCTCCGACACTGAGGGTCTTGTAAAGAGTCTGCCTCTGGATCTCACC
 AGGGCCCAGTCATATATGCACAGTTAGACCACTCCGGCGGACATCACAGTGACAAGATTAAC
 AAGTCAGAGTCGTGGTGTATGCGGATATCCGAAAGAAT**TAA**GAGAACATCTAGAACATATC
 CTCAGCAAGAAACAAACCAACTGGACTCTCGTGCAGAAAATGTAGCCCATTACCACATGT
 AGCCTTGGAGACCCAGGAAGGACAAGTACACGTGTAACAGAGGGAGAGAAAGATGTGT
 ACAAAAGGATATGTATAAATATTCTATTAGTCATCCTGATATGAGGAGCCAGTGTGATGA
 TGAAAAGATGGTATGATTCTACATATGTACCCATTGTCTGCTGTTTGTACTTCTTT
 AGGTCAATTACAATTGGGAGATTTCAGAAACATTCCCTTCACCATCATTAGAAATGGTTG
 CCTTAATGGAGACAATAGCAGATCCTGTAGTATTCCAGTAGACATGGCCTTTAATCTAAG
 GGCTTAAGACTGATTAGTCTTAGCATTACTGTAGTTGGAGGATGGAGATGCTATGATGGAA
 GCATACCCAGGGTGGCCTTACAGTACGATCAGTACCTTATTGTCTGCCGCTTTAAAAA
 AATACCCATTGGCTATGCCACTTGAAAACAATTGAGAAGTTTTGAAGTTTCTCACT
 AAAATATGGGCAATTGTTAGCCTACATGTTGTAGACTTACTTTAAGTTGCACCCCTG
 AAATGTGTATCAATTCTGGATTCAATAGCAAGATTAGCAAAGGATAAATGCCGAAG
 GTCACTTCATTCTGGACACAGTGGATCAATACTGATTAAGTAGAAAATCCAAGCTTGCTT
 GAGAACTTTGTAAACGTGGAGAGTAAAAGTATCGGTTTA

FIGURE 212

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76510
><subunit 1 of 1, 269 aa, 1 stop
><MW: 29082, pI: 9.02, NX(S/T): 3
MAASAGAGAVIAAPDSRRWLWSVLAAALGLLTAGVSALEVYTPKEIFVANGTQGKLTCKFKS
TSTTGGLTSWSFQPEGADTTVSFFHYSQGQVYLGNYPPFKDRISWAGDLDKKDASINEN
MQFIHNGTYICDVKNPPDIVVQPGHIRLYVVEKENLPVFPVVVVGIVTAVVLGLTLLISMI
LAVLYRRKNSKRDYTGCSTSESLSPVKQAPRKSPSDTEGLVKSLSHQQGPVIYAQLDHSG
GHHSDKINKSESVVYADIRKN
```

Signal peptide:

amino acids 1-37

Transmembrane domain:

amino acids 161-183

FIGURE 213

GCCGGCTGTGCAGAGACGCC **ATG**TACCGGCTCCTGTCAGCAGTGACTGCCCGGGCTGCCGCC
 CCCGGGGCTTGGCCTCAAGCTGCGGACGACGCCGGGTCCATCAGCGGCCGGCTGCCGCC
 TCTCGGCCACGGCTGGGTGGGGCTCGGGCTGGGTGGGGCTGGCGCTGGGTGAAGC
 TGGCAGGTGGGCTGAGGGCGCGCCCCGGCGCAGTCCCCCGGGCCCCGACCCTGAGGCG
 TCGCCTCTGGCCGAGCCGCCACAGGAGCAGTCCCTGCCCGTGGTCTCCGCAGACCCGGC
 GCCGCCCTGCTCCAGGTGCTCGCCAGAGCCATCGAGAGCAGCCGCACCTGCTGCACAGGA
 TCAAGGATGAGGTGGCGCACCGGCATAGTGGTTGGAGTTCTGTAGATGGAAAAGAAGTC
 TGGTCAGAAGGTTAGTTATGCTGATGTTGAGAACCGTGTACCATGTAACCAGAGACAGT
 TATGCGAATTGCTAGCATCAGCAAAAGTCTCACCATGGTGCTCTGCCAAATTGTGGGAAG
 CAGGGAAACTGGATCTTGATATTCCAGTACAACATTATGTTCCGAATTCCCAGAAAAAGAA
 TATGAAGGTGAAAAGGTTCTGTCACAACAAGATTACTGATTCCCATTAAAGTGGATTGCG
 TCATTATGAAAAGGACATAAAAAGGTGAAAGAAGAGAAAGCTTATAAAGCCTGAAGATGA
 TGAAAGAGAATGTTGCATTGAGCAAGAAAAGAAGGCAAAAGTAATGAAAAGAATGATTG
 ACTAAATTAAAACAGAGCAGGAGAATGAAGCCAATGCCGAATTCAAAACCTGGCAAGAA
 AAAGAATGATTGAAACAAGGCGAATTATTTGAGAGAAAAGTTGAAAATTCAATTGAAT
 CCCTAACGATTATTTAAAATGATCCTTGTCTCAAACCTGGTAGTCAGTTTGATATTCA
 ACTTTGGCTATACCCTACTGGCAGCCATAGTAGAGAGAGCTCAGGATGTAATATTGGA
 CTATATGCAGAAAATATTCCATGACTGGATATGCTGACGACTGTGCAGGAAGAAAACGAGC
 CAGTGATTACAATAGAGCAAGG**TAA**ATGAATACTTCTGCTGTCTAGCTATATCGC
 TTAACACTATTTATTAATTAAAAGTCAAATTTCTTGTTCATTCCAAAATCAACCTGC
 CACATTGGGAGCTTCTACATGTCTGTTCTCATCTGTAAGTGAAGGAAGTAAAACA
 TGTTTATAAGTAAAAAAA

FIGURE 214

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76522
><subunit 1 of 1, 373 aa, 1 stop
><MW: 41221, pI: 8.54, NX(S/T): 0
MYRLLSAVTARAAAPGGLASSCGRRGVHQAGLPPPLGHGWVGGLGLGLALGVKLAGGLRG
AAPAQSPAAPDPEASPLAEPPEQQSLAPWSPQTPAPPSCRCFARAIESSRDLLHRIKDEVGA
PGIVVGVSVDGKEVWSEGLGYADVENRVPCKPETVMRIASISKSLTVALAKLWEAGKLDLD
IPVQHYVPEFPEKEYEGEKVSVTRLLISHLSGIRHYEKDIKKVKEEKAYKALKMMKENVAF
EQEKEGKSNEKNDFTKFKTEQENEAKCRNSKPGKKNDFEQGELYLREKFENSIESLRLFKN
DPLFFKPGSQFLYSTFGYTLLAAIVERASGCKYLDYMQKIFHDLDMLTTVQEENEPVIYNRAR
```

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 39-60

FIGURE 215

GTGACACTATAGAAGAGCTATGACGTCGCATGCACCGTACGTAAGCTCGAACCGCTCG
 AGGCTGGTGGAAAGAACCGAG**ATG**GCAGCCAGCGCTGGGCAACCCGGCTGCTCCTGC
 TCTTGCTGATGGCGGTAGCAGCGCCAGTCGAGGCCGGGAGCGGCTGCCGGCCGGACT
 GGTGCGCGAGGGCTGGGCGGAAGGTCGAGAGGGCAGGCCGTGGCACGGTGGGCTGCT
 GCTGGAGCACTCATTTGAGATCGATGACAGTGCCAACCTCCGGAACGGGGCTCACTGCTCT
 GGAACCAGCAGGATGGTACCTTGTCCCTGTCACAGCGCAGCTCAGCGAGGAGGAGCAGGGC
 CGACTCCGGATGTGGCAGCCCTGAATGGCCTGTACCGGGTCCGGATCCCAAGGCGACCCGG
 GGCCCTGGATGGCCTGGAAGCTGGTGGCTATGTCTCCTCCTTGTCCCTGCGTGTCCCTGG
 TGGAGTCGCACCTGTCGGACCACTGACCCCTGCACGTGGATGTGGCCGGAACGTGGTGGC
 GTGTCGGTGGTACGCACCCCGGGGCTGCCGGGCCATGAGGTGGAGGACGTGGACCTGGA
 GCTGTTCAACACCTCGGTGCAGCTGCAGCCGCCACACAGCCCCAGGCCCTGAGACGGCGG
 CCTTCATTGAGCGCCTGGAGATGGAACAGGCCAGAAGGCAAGAACCCCCAGGAGCAGAAG
 TCCTTCTCGCCAAATACTGGATGTACATCATTCCGTCGTCCCTGTTCTCATGATGTCAGG
 AGCGCCAGACACCGGGGCCAGGGTGGGGTGGGGGTGGGTGGTGGGGTAGTGGCC
 TTTGCTGTGTGCCACCCCTCCCTG**TAA**GTCTATTTAAAAACATCGACGATACTTGAAATGTG
 TGAACGTTTGAAGCTACAGCTTCCAGCAGCCAAAGCAACTGTTGTTGGCAAGACGG
 TCCTGATGTACAAGCTTGATTGAAATTCACTGCTCACTGATACTGTTATTGAAACCCAAG
 GAATGGCTGTCCCCATCCTCATGTGGCTGTGGAGCTCAGCTGTGTGTGGCAGTTAT
 TAAACTGTCCCCAGATCGACACGAAAAAAAAAA

FIGURE 216

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76529
><subunit 1 of 1, 269 aa, 1 stop
><MW: 28004, pI: 5.80, NX(S/T): 1
MAAASAGATRLLLLLLMAVAAPSRARGSGCAGTGARGAGAEGREGEACGTVGLLLEHSFEI
DDSANFRKRGSLWNQQDGTLSLSQRQLSEEERGRLRDVAALNGLYRVRIPRPGALDGLEA
GGYVSSFVPACSLVESHLSDQLTLHVDVAGNVVGVSVVTHPGGCRGHEVEDVDLELFNTSVQ
LQPPTTAPGPETAAFIERLEMEQAQKAKNPQEOKSFFAKYWMYIIIPVVLFLMMMSGAPDTGGQ
GGGGGGGGGGGGSGLCCVPPSL
```

Signal peptide:

amino acids 1-24

Transmembrane domain:

amino acids 226-243

FIGURE 217

GGAGCGCTGCTGGAACCCGAGCCGGAGCCGAGCACAGCAGGGAGGGTGGCCTGGCGGCCT
 GGAGCCGGACGTGTCCGGGGCGTCCCCGAGACCGGGGCAGCAGGTGTCCTGGCCTGGGGCTGGAACT
ATGCTGGTACTGCCTACCTGCTTTGTAGGCCTCCTGGCCTCCTGCCTGGGGCTGGAACT
 GTCAAGATGCCGGCTAAACCCCTGGAAGGGCCTGCAGCAATCCCTCCTCCTCGGTTTC
 AACTGGACTTCTATCAGGTCTACTCCTGGCCCTGGCAGCTGATTGGCTTCAGGCCCCCTAC
 CTCTATAAAACTCTACCAGCATTACTACTCCTGGAAGGTCAAATTGCCATCCTATGTCTG
 TGGCCTGCCTCTACAGCCTCTTGGCCTAGTGGCCTCCTCCCTGTGGATTGGCTGGTC
 GCAAGAATTCTTGTGTCTCTTCTCCCTGACTTAACCTACTCATGCTGCTAACCAAACTCTCT
 CAAGACTACTTGTGCTGCTAGTGGGGCGAGCACTGGTGGGCTGTCCACAGCCCTGCTCTT
 CTCAGCCTCGAGGCCTGGTATATCCATGAGCACGTGGAACGGCATGACTTCCCTGCTGAGT
 GGATCCCAGCTACCTTGCTCGAGCTGCCTCTGGAACCATGTGCTGGCTGTAGTGGCAGGT
 GTGGCAGCTGAGGCTGTAGCCAGCTGGATAGGGCTGGGCCTGTAGCGCCCTTGTGGCTGC
 CATCCCTCTCCCTGGCTCTGGCAGGGCCTGGCCCTCGAAACTGGGGGAGAACTATGACC
 GGCAGCGTGCCTCTCAAGGACCTGTGCTGGAGGCCTGCGCTGCCTCCTGTGGACCGCCGC
 GTGCTGCTGGCACCATAAGCTCTATTGAGAGTGTCACTTCATCTTGTCTTCCCT
 CTGGACACCTGTGCTGGACCCACACGGGGCCCTCTGGCATTATCTCCAGCTTCATGG
 CAGCCAGCCTGCTGGCTTCCCTGTACCGTATGCCACCTCCAAGAGGTACCACCTTCAG
 CCCATGCACCTGCTGTCCCTGCTGTGCTCATCGTCGTCTCTCTTCATGTTGACTTT
 CTCTACCAGCCCAGGCCAGGAGAGTCCGGTGGAGTCCTCATAGCCTTCTACTTATTGAGT
 TGGCTTGTGGATTATACTTCCAGCATGAGCTTCTACGGAGAAAGGTGATCCCTGAGACA
 GAGCAGGCTGGTACTCAACTGGTCCGGGTACCTCTGCACTCACTGGCTGCCTAGGGCT
 CCTTGTCCCTCATGACAGTGATCGAAAAACAGGCACTCGAATATGTCAGCATTGCTCTG
 CTGTCATGGTGTGGCTCTGCTGGCAGTGGTGGACTCTTACCGTGGTAAGGCATGATGCT
 GAGCTGGGGTACCTCACCTACTGAGGAGCCATGCCCTGAGCTG**TAA**CCCCACTCCAG
 GACAAGATAGCTGGACAGACTCTGAATTCCAGCTATCCGGATTGTACAGATCTCTGT
 GACTGACTTTGTGACTGTCCTGTGGTTCTCCTGCCATTGCTTGTGTTGGAGGACATGA
 TGGGGGTGATGGACTGGAAAGAAGGTGCCAAAAGTCCCTCTGTGTTACTCCCATTAGAAA
 ATAAACACTTTAAATGATCAAAAAAAAAAA

FIGURE 218

MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDFYQVYFLALAADWILQAPY
LYKLYQHYYFLEGQIAILYVCGILASTVLFGLVASSLVWDLGRKNSCVLFSLTYSLCCLTKLS
QDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAFAFWNHVLAVVAG
VAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGLRCLLSDRR
VLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIIFSSFMAASLLGSSLYRIATSKRYHLQ
PMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPSMSFLRRKVIPET
EQAGVLNWFRVPLHSLACGLLVLHDSDRKTGTRNMFSICSAVMVMALLAVVGLFTVVRHDA
ELRVPSPTEEPYAPEL

Signal peptide:

amino acids 1-18

Transmembrane domain:

amino acids 41-55, 75-94, 127-143, 191-213, 249-270, 278-299,
314-330, 343-359, 379-394, 410-430

FIGURE 219

GCGACGCGCGGGCGGGCGAGAGGAAACGCGGCCGGCCGGCCCTGGAG**ATG**
 GTCCCCGGCGCCGCGGGCTGGTGTCTCGTCTGGCTCCCCGCGTCGCGGCCA
 CGGCTCCGTATCCATGATTATTGTACTTCAAGTGCTGAGTCCTGGGACATTGATACA
 TCTTCACAGCCACACCTGCCAAGGACTTGGTGGTATCTTCACACAAGGTATGAGCAGATT
 CACCTGTCCCCGCTGAACCTCCAGAGGCCTGCAGGGAACTCAGCAACGGTTCTCATCCA
 GGACCAGATTGCTCTGGTGGAGAGGGGGGCTGCTCCTCTCCAAGACTCGGGTGGTCC
 AGGAGCACGGCGGGCGGTGATCATCTCTGACAACGCAGTGACAATGACAGCTTCTAC
 GTGGAGATGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTTTCTGCTCGG
 CCGAGACGGCTACATGATCCGCCGCTCTGGAACAGCATGGGCTGCCATGGCCATCATT
 CCATCCCAGTCAATGTCACCAGCATCCCCACCTTGAGCTGCTGCAACCGCCCTGGACCTTC
 TGG**TAG**AAGAGTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCC
 AGGAATTTGCTACTTGAATTGGAGATAGCATCTGGGACAAGTGGAGCCAGGTAGAGGA
 AAAGGGTTGGCGTTGCTAGGCTGAAAGGGAAAGCCACACCACTGGCCTCCCTCCCCAGG
 GCCCCCAAGGGTGTCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCTGGCTCTGGCTA
 GAACCCGAAACAAAAGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTACACT
 CACCTGGCTCCAGCCTCCCTACCCAGGGTCTCTGCACAGTGACCTCACAGCAGTTGG
 AGTGGTTAAAGAGCTGGTGTGGGACTCAATAAACCTCACTGACTTTAGCAATAAA
 GCTTCTCATCAGGGTTGCAAAAAAAAAAAAAAAA

FIGURE 220

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIHDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQ
IHLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVDNDSF
YVEMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIIISIPVNVTSIPTFELLQPPWTFW
```

Signal peptide:

amino acids 1-20

FIGURE 221

TCTGCCTCCACTGCTCTGTGCTGGGATC**ATG**GAACTTGCACTGCTGTGTGGCTGGTGGTGA
TGGCTGGTGTGATTCCAATCCAGGGCGGGATCCTGAACCTGAACAAGATGGTCAAGCAAGTG
ACTGGGAAATGCCCATCCTCTCCTACTGGCCCTACGGCTGTCAGTGCAGACTAGGTGGCAG
AGGCCAACCAAAGATGCCACGGACTGGTGCTGCCAGACCCATGACTGCTGCTATGACCACC
TGAAGACCCAGGGTGCAGCATCTACAAGGACAACAACAAAAGCAGCATACTGTATGGAT
TTATCTCAACGCTATTGTTAATGGCTGTGTTAATGTGATCTATCTGGAAATGAGGACTC
CGAA**TAA**AAAGCTATTACTAWTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAA

FIGURE 222

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76538
><subunit 1 of 1, 116 aa, 1 stop
><MW: 12910, pI: 6.41, NX(S/T): 1
MELALLCGLVVMAGVIPIQGGILNLNKMVKQVTGKMPILSYWPYGCCHCGLGGRGQPKDATDW
CCQTHDCCYDHLKTQGCGIYKDNNKSSIHCMDLSQRYCLMAVFNVIYLENEDSE
```

Important features of the protein:

Signal peptide:

amino acids 1-17

Transmembrane domain:

amino acids 1-24

N-glycosylation site.

amino acids 86-89

N-myristoylation sites.

amino acids 20-25, 45-50

Phospholipase A2 histidine active site.

amino acids 63-70

FIGURE 223

CTCGCTTCTCCTCTGGATGGGGGCCAGGGGCCAGGAGAGTATAAGGCATGTGGAG
GGTCCCCGACAACCAAGACGCCAGTCACAGGCAGAGCCCTGGG**ATG**CACCGGCCAGAGG
CCATGCTGCTGCTCACGCTGCCCTCCTGGGGGCCACCTGGCAGGAAGATGTAT
GCCCTGGAGGAGGCAAGTATTCAGCACCCTGAAGACTACGACCATGAAATCACAGGGCT
GCGGGTGTCTGTAGGTCTCTGGTAAAAGTGTCCAGGTGAAACTGGAGACTCCTGGG
ACGTGAAACTGGAGCCTAGGTGGAAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATAC
ATCACAAAAGTCTTGTGCCTTCCAAGCTTCCTCCGGGTATGGTCATGTACACCAGCAA
GGACCGCTATTCTATTGGAAAGCTTGATGGCCAGATCTCCTCTGCCTACCCAGCCAAG
AGGGCAGGTGCTGGTGGCATCTATGCCAGTATCAACTCCTGGCATCAAGAGCATGGC
TTTGAATGGAATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTC
AGCAAACTCACCGTGGTCGC**TAG**GGTGGGTATGGGCCATCCGAGCTGAGGCCATCTGT
GTGGTGGTGGCTGATGGTACTGGAGTAAGTGAGTCGGACGCTGAATCTGAATCCACCAATA
AATAAAGCTTCTGCAGAAAA

FIGURE 224

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSGLLLKVSVQVK
LGDSWDVKGALGGNTQEVTLQPGEYITKVFVAFQAFLRGMVMTSKDRYFYFGKLDGQISS
AYPSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTEPPVNLTYSANS PVGR
```

Signal peptide:

amino acids 1-22

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22

FIGURE 225

GCTGAGCGTGTGCGCGGTACGGGGCTCTCCTGCCTCTGGGCTCCAACGCAGCTCTGTGGCT
 GAACTGGGTGCTCATCACGGGAAC TGCTGGCTATGGAATACAGATGTGGCAGCTCAGGTAG
 CCCCAAATTGCCTGGAAGAACATACATGTTTCGATAAGAAGAACATTGTAAGGATCCAGTT
 TTTTTTTAACCGCCCCCTCCCCACCCCCAAAAAAACTGTAAAGATGCAAAAACGTAATAT
 CCATGAAGATCCTATTACCTAGGAAGATTTGATGTTTGCTGCGAATGCGGTGTTGGATT
 TATTTGTTCTGGAGTGTCTCGGTGGCTGGCAAGAACATAATGTTCAAAATCGGTCCATCT
 CCCAAGGGTCCAATTTCCTGGGTGTCAGCGAGCCCTGACTCACTACAGTGCAGCTG
 ACAGGGCTGTCACTGCAACTGGCCCCTAACGCCAAAGCAAAAGACCTAACGGACGACCTTGAA
 CAATACAAAGG**ATG**GGTTCAATGTAATTAGGCTACTGAGCGGATCAGCTGTAGCACTGGTT
 ATAGCCCCACTGTCTACTGACAATGCTTCTGCCGAACGAGGATGCCCTAACGGCTG
 TAGGTGTGAAGGCAAAATGGTATATTGTGAATCTCAGAACATTACAGGAGATACCCCTCAAGTA
 TATCTGCTGGTTGCTTAGGTTGCTCCCTGCTATAACAGCCTCAAAACTTAAGTATAAT
 CAATTAAAGGGCTAACCAGCTCACCTGGCTATACTTGACCATAACCATAACGAAATAT
 TGACGAAAATGCTTTAATGGAATACGCAACTAACAGAGCTGATTCTTAGTCCAATAGAA
 TCTCCTATTTCCTAACAAATACCTTCAGACCTGTGACAAATTACGGAACTTGGATCTGTCC
 TATAATCAGCTGCATTCTCTGGATCTGAACAGTTGGGGCTTGCAGGAAAGCTGCTGAGTT
 ACATTACGGCTAACCTCCCTGAGAACCATCCCTGCGAATATTCCAAGACTGCCGCAACC
 TGGAACTTTGGACCTGGGATATAACCGGATCCGAAGTTAGCCAGGAATGTCTTGCTGGC
 ATGATCAGACTCAAAGAACTTCACCTGGAGCACAATCAATTTCAGCTAACCTGGCCCT
 TTTCCAAGGTTGGTCAGCCTTCAGAACCTTACTTGCAGTGGAAATAAAATCAGTGTCA
 GACAGACCATGCTGGACCTGGAGCTCCCTACAAAGGCTTGATTATCAGGCAATGAGATC
 GAAGCTTCAGTGGACCCAGTGTGTTCCAGTGTGTCCTGAATCTGCAGCGCCTAACCTGGA
 TTCCAACAAGCTCACATTATTGGTCAAGAGATTGGATTCTGGATATCCCTCAATGACA
 TCAGTCTGCTGGGAATATGGGAATGCAGCAGAACATTGCTCCCTGTAAACTGGCTG
 AAAAGTTAAAGGTCTAAGGGAGAACATCAATTATCTGTGCCAGTCCCAAAGAGCTGCAAGG
 AGTAAATGTGATCGATGCAGTGAAGAACACTACGCATCTGTGGCAAAAGTACTACAGAGAGGT
 TTGATCTGCCAGGGCTCTCCAAAGCCACGTTAACGCCAACGCTCCCCAGGCCGAAGCAT
 GAGAGCAAACCCCTTGGCCCCGACGGTGGAGCCACAGAGGCCAGAGACCGATGC
 TGACGCCGAGCACATCTCTTCCATAAAATCATCGCGGGCAGCGTGGCGCTTCTGTCCG
 TGCTCGTCATCCTGCTGGTTATCTACGTGTCACTGGAAAGCGGTACCTGCGAGCATGAAGCAG
 CTGCAGCAGCGCTCCCTCATGCGAACAGGAAAGAACAGTCCCTAAAGCAAAT
 GACTCCCAGCACCCAGGAATTATGTAGATTATAAACCCACCAACACGGAGACCAGCGAGA
 TGCTGCTGAATGGGACGGGACCCCTGCACCTATAACAAATGGGCTCCAGGGAGTGTGAGGTA
TGAACCATTGTGATAAAAAGAGCTCTTAAAGCTGGAAATAAGTGGTGTGTTATTGAACTC
 TGGTGAATCAAGGGAACCGCGATGCCCTCCCTCCCTCTCCCTCACTTGGTGG
 CAAGATCCTCCTGTCCGTTAGTGCATTCAATAACTGGTCATTTCCTCATACATA
 ATCAACCCATTGAAATTAAATACCACAAATCAATGTGAAGCTTGAACCTCGGTTAATATAA
 TACCTATTGTATAAGACCCCTTACTGATTCCATTAAATGTCGCATTGTTAAGATAAAACT
 TCTTCATAGGTAAAAAAAAAA

FIGURE 226

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77301
><subunit 1 of 1, 513 aa, 1 stop
><MW: 58266, pI: 9.84, NX(S/T): 4
MGFN VIRLLSGSAVALVIAPTVLLTMLSSAERGCPKGCRCEGK MVYCESQKLQEIPSSISAG
CLGLSL RYNSLQKLKYNQFKGLNQLTWLYLDHNHISNIDENAFNGIRRLKELILSSNRISYF
LNNTFRPVTNLRNLDLSYNQLHSLGSEQFRGLRKLLSLHLRSNSLRTIPVRI FQDCRNLELL
DLGYNRIRSLARNVFAGMIRLKELHLEHNQFSKLNLALFPRLVSLQNLQWNKISVIGQTM
SWTWSSLQRLLDLSGNEIEAFSGPSVFQCVPNLQRLNLDNKLTFIGQEILD SWISLNDISLA
GNIWECSRNICSLVNWLKSFKGLRENTI ICASPKELQGVNVIDAVKNYSICGKSTTERFDLA
RALPKPTFKPKLPRPKHESKPPLPPTVGATEPGPETDADAEHISFHKIIAGSVALFLSVLVI
LLVIYVSWKRYPASMKQLQQRSLMRRHRKKRQSLKQMTPSTQEFYVDYKPTNTETSEMLLN
GTGPCTYNKSGSRECEV
```

Important features of the protein:**Signal peptide:**

amino acids 1-33

Transmembrane domain:

amino acids 420-442

N-glycosylation sites.

amino acids 126-129, 357-360, 496-499, 504-507

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 465-468

Tyrosine kinase phosphorylation site.

amino acids 136-142

N-myristoylation sites.

amino acids 11-16, 33-38, 245-250, 332-337, 497-502, 507-512

FIGURE 227

AGTTCTGAGAAAGAAGGAAATAAACACAGGCACCAAACCACTATCCTAAGTTGACTGTCC
 TAAATATGTCAAGATCCAGACTTTCAGTGTACCTCAGCGATCTAACGATAGGGATCTTG
 TGTTGCCGCTATTCCAGTTGGTCTCTCGGACCTACCATGCGAAGAAGATGAAATGTGT
 AAATTATAATGACCAACACCCTAATGGCTGGTATATCTGGATCCTCCTGCTGCTGGTTTGG
 TGGCAGCTCTCTGTGGAGCTGTGGTCTCTGCCTCCAGTGCTGGCTGAGGAGACCCGA
 ATTGATTCTCACAGGCACCATGGCAGTTTGCTGGAGACTGGACTCTATTATGG
 GACAGAAGCAGCTGTGAGTCCAATGTTGGAATTACCTTCAAACCTCAAACCCCTGACCTAT
 ATCCTGTTCTGCTCCATGTTGCCCTTAGGCTCCCCACCTCCATATGAAGAAATTGTA
 AAAACAACCTGATTTAGGTGTGGATTATCAATTAAAGTATTAACGACATCTGTAATTCCA
 AACATCAAATTAGGAATAGTTATTCAGTTGGAAATGTCCAGAGATCTATTATATA
 GTCTGAGGAAGGACAATTGACAAAAGAATGGATGTTGGAAAAAAATTGGTCACTGGAGATG
 TTTAAATAGTAAAGTAGCAGGCTTGTGTCAGTGTACTGCTGTATCATACTTTATGCTACAC
 AACCAAATTATGCTTCTCCACTAGTATCCAAACAGGCAACAATTAGGTGCTGGAAGTAGTT
 TCCATCACATTAGGACTCCACTGCAGTATACAGCACACCATTCTGCTTAAACTCTTC
 CTAGCATGGGTCCATAAAATTATAATTAAACATAGCCCAAGCCGAGAATCCAACAT
 GTCCAGAACAGAACCAAGAAAGATAGTATTGAATGAAGGTGAGGGGAGAGAGTAGGAAAAA
 GAAAAGTTGGAGTTGAAGGGTAAAGGATAATGAAGAGGAAAAGGAAAGATTACAAGTCT
 CAGCAAAACAAGAGGTTTATGCCCAACCTGAAGAGGAAGAAATTGTAGATAGAAGGTGA
 AGGAGATTGCTGAAGATATAGAGCACATATAATGCCAACACGGGAGAAAAGAAAATTCCC
 CTTTACAGTAATGAATGTGGCCTCCATAGTCATAGTGTCTCTGGAGCCTCAGGGCTTG
 GCATTATTGCAGCATCATGCTAACGACCTCGGCATAGGTATCTGTTCCATGAGGACTGC
 AGAAGTAGCAATGAGACATCTCAAGTGGATTGGCAGTGGCCATCAGCAGGGGACAGA
 CAAAAACATCCATCACAGATGACATATGATCTCAGCTGACAAATTGTTGAACAAAACAAT
 AACATCAATAGATATCTAAAAA

FIGURE 228

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77303
><subunit 1 of 1, 146 aa, 1 stop
><MW: 16116, pI: 4.99, NX(S/T): 0
MSRSRLFSVTSAISTIGILCLPLFQLVLSDLPCEEDEMCVNNDQHPNGWYIWILLLLVLVA
ALLCGAVVLCLQCWLRRPRIDSHRRTMAVFAVGDLDSIYGTEAAVSPVGIIHLQTQTPDLYP
VPAPCFGPLGSPPPYEEIVKTT
```

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 52-70

FIGURE 229

GAGC GGAG TAAATCTCCACAAGCTGGGAACAAACCTCGTCCCAACTCCCACCCACC GGCGT
 TTCTCCAGCTCGATCTGGAGGCTGCCAGTGTGGGACGCAGCTGACGCCCGCTTATT
 GCTCTCGCTCGCGCCCGGCTCAGAAGCTCCGTGGCGCGCGACCGTGACGAGAACGCC
 ACGGCCAGCTCAGTTCTACTTTGGGAGAGAGAGAAAGTCAGATGCCCTTTAAACT
 CCCTCTCAAACATCTCCTGGGTGACTGAGTTAATAGAGTGGATACAACCTGCTGAAG
 ATGAAGAATATAACATATTGAGGATATTTTTCTTTCAAGTCTTGATTTGTGGC
 TTACCTCAAGT TACCATTTTCAGTCAGTCTGTTGTTGCTTCTTCAGAA**ATG**TTTTTA
 CAATCTCAAGAAAAAATATGTCCCAGAAATTGAGTTACTGTTGCTTGTATTGGACTCATT
 TGGGGATTGATGTTACTGCACTATACTTTCAACAAACCAAGACATCAAAGCAGTGTCAAGTT
 ACGTGAGCAAATACTAGACTTAAGCAAAAGATATGTTAAAGCTCTAGCAGAGGAAAATAAGA
 ACACAGTGGATGTCGAGAACGGTCTATGGCAGGATATGCGGATCTGAAAAGAACAAATT
 GCTGTCCTCTGGATGACATTTGCAACGATTGGTGAAGCTGGAGAACAAAGTTGACTATAT
 TGTGGAATGGCTCAGCAGCCACACCAATGGTACTAGTGGGAATTGGTGCCAGTAA
 CCACAAATAAAAGAACGAATGTCCTGGGCAGTATCAGA**TAG**CAGTTGAAAATCACCTGTGC
 TGCTCCATCCACTGTGGATTATACCTATGGCAGAAAAGCTTATAATTGCTGGCTTAGGAC
 AGAGCAAACTTACAATAAAAGCTCTACACATTTCAGGAGTATGCTGGATTATGGAAC
 TCTAATTCTGTACATAAAATTTAAAGTTATTGTTGCTTCAGGCAAGTCTGTTCAATG
 CTGTAATGTCCTTAAAGAGAATTGGTAACCTGGTTGATGTGGTAAAGCAGATAGGTGAGT
 TTTGTATAATCTTTGTGTTGAGATCAAGCTGAAATGAAAACACTGAAAACATGGATT
 ATTTCTATAACACATTATAAGTATATAACACGTTTTGGACAAGTGAAGAATGTTAA
 TCATTCTGTCAATTGTTCTCAATAGATGTAACCTGTTAGACTACGGCTATTGAAAAAATGTG
 CTTATTGTACTATATTGTTATTCCAATTATGAGCAGAGAACAGGAAATATAATGTTGAAA
 TAATGTTTGAAATCATGACCCAAAGAACATGATTGATTGACTATCCTCAGAATAACTGA
 AGGTTAATTATTGTATTTAAAAATTACACTTATAAGAGTATAATTGAAATGGGTAG
 CAGCCACTGTCCATTACCTATCGTAACATTGGGCAATTAAATAACAGCATTAAAATAGTT
 GTAAACTCTAATCTTATAACTTATTGAAGAATAAAAGATATTGATGAGAGTAACAATA
 AAGTATTGATTTCACATACATGAATGTTCAATTAAAGTTAATCCTTGAGTGTCT
 ATGCTATCAGGAAAGCACATTATTCCATATTGGGTTAATTGCTTTATTATATTGGTC
 TAGGAGGAAGGGACTTGGAGAATGGAACCTTGAGGACTTGTAGCCAGGTATATAATAAA
 GGTACTTTGTGCTGCATTAAATTGCTTGAAAGTGTAAACATTATATTATAAGAGTATC
 CTTTATGAAATTGTAATTGATACAGATGCATTAGATATTCAATTATATAATGGCAC
 TTAAAATAAGAACATTAAAATAAAACTATGAAGATTGACTATCTTTCAGGAAAAAGCT
 GTATATAGCACAGGGAACCTAATCTGGGTAAATTCTAGTATAAAACAAATTATACTTTAT
 TTAAATTCCCTGTAGCAAATCTAATTGCCACATGGTGCCTATATTCAAGTATT
 CTCTATAGTAACTGCTTAAGTGCAGCTAGCTTAGACTATATAGAATTAGATAT
 TGTATTGTTCGTCATTATAATATGCTACCACATGTAGCAATAATTACAATATT
 TAAATATGTGAAATATTGTTCATGAAAGACAGATTCCAATCTCTTCTCTGT
 CTGTCTACCTTATGTGAAGAAATTAAATTATGCCATTGCCAGGT

FIGURE 230

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77648
><subunit 1 of 1, 140 aa, 1 stop
><MW: 15668, pI: 10.14, NX(S/T): 5
MFFTISRKNMSQKLSLLLLVFGLIWGLMILLHYTFQQPRHQSSVKLREQILDLSKRYVKALAE
ENKNTVDVENGASMAGYADLKRTIAVLLDDILQRLVKLENKVDYIVVNGSAANTTNGTSGNL
VPVTTNKRTNVSGSIR
```

Important features of the protein:

Signal peptide:

amino acids 1-26

FIGURE 231

CGCGGGCCGGGCCGCGGGGTGAGCGTGCCGAGGCGGCTGTGGCGCAGGCTTCCAGCCCCCAC
CATGCCGTGGCCCCTGCTGCTGCTGCCGTGAGTGGGGCCCAGACAACCGGCCATGCT
 TCCCCGGGTGCCAATGCAGGGTGGAGACCTTCGGGCTTTGACAGCTTCAGCCTGACTCGG
 GTGGATTGTAGCGGCCTGGGCCCCACATCATGCCGGTGCCCATCCCTCTGGACACAGCCC
 CTTGGACCTGTCCCTCCAACCAGCTGGAGATGGTGAATGAGTCGGTGTGGCGGGCGGGCT
 ACACGACGTTGGCTGGCTGGATCTCAGCCACAACCTGCTCACCAAGCATCTCACCCACTGCC
 TTCTCCCGCCTCGTACCTGGAGTCGCTGACCTCAGCCACAATGCCCTGACAGCCCTGCC
 AGCGAGAGCTTCACCAGCTCACCCCTGAGCGACGTGAACCTTAGCCACAACCAGCTCCGG
 AGGTCTCAGTGTCTGCCTCACGACGCACAGTCAGGGCGGGCACTACACGTGGACCTCTCC
 CACAACCTCATTCACCGCCTCGTGGCCCACCCACGAGGGCGGCCCTGCCTGCGCCCACCAT
 TCAGAGCCTGAACCTGGCCTGGAACCGGCTCCATGCCGTGCCAACCTCCGAGACTTGGCCC
 TGCGCTACCTGAGCCTGGATGGAACCCCTAGCTGTATTGGTCCGGTGCCTCGGGGG
 CTGGGAGGCCTACACACCTGTCTGGCCAGCCTGCAGAGGCTCCCTGAGCTGGCGCCAG
 TGGCTCCGTGAGCTACCGGGCTGCAGGTCTGGACCTGTCGGGCAACCCAAAGCTTAAC
 GGGCAGGAGCTGAGGTGTTTCAGGCCTGAGCTCCCTGCAGGAGCTGGACCTTCGGGCACC
 AACCTGGTGCCCTGCCTGAGGCGCTGCTCCACCTCCGGCACTGCAGAGCGTCAGCGT
 GGGCCAGGATGTGGTGGCCCTGGGAGGGCACCTACCCCCGGAGGCCTGGCT
 CCAGCCCCAAGGTGCCCTGCACTGCAGACACCCGGGAATCTGCTGCCAGGGGCCACC
 ATCTTG**TGA**CAAATGGTGTGGCCCAGGGCACATAACAGACTGCTGTCTGGCTGCCTCAG
 GTCCCGAGTAACCTATGTTCAATGTGCCAACACCAAGTGGGGAGGCCAGGCCTATGTGGCA
 GCGTACCCACAGGAGTTGTGGCCTAGGAGAGGCTTGGACCTGGGAGGCCACACCTAGGAGC
 AAAGTCTCACCCCTTGCTACGTTGCTTCCCAAACCATGAGCAGAGGGACTTCGATGCCA
 AACCAGACTCGGGTCCCCTGCCTGCTCCCTCCCCACTTATCCCCAAGTGCCTCCCTCAT
 GCCTGGGCCGGCTGACCGCAATGGCAGAGGGTGGGTGGGACCCCTGCTGCAGGGCAGA
 GTTCAGGTCCACTGGGCTGAGTGTCCCCTGGGCCATGGCCAGTCACTCAGGGCGAGTT
 TCTTTCTAACATAGCCCTTCTTGCCATGAGGCCATGAGGCCGCTTCATCCTTCTAT
 TTCCCTAGAACCTTAATGGTAGAGGAATGCAAAGAATCAAGTCCACCCCTCATGTGAC
 AGATGGGGAAACTGAGGCCCTGAGAAGGAAAAGGCTAATCTAAGTTCCTGCGGGCAGTGGC
 ATGACTGGAGCACAGCCTCTGCCTCCCAGCCGGACCCAAATGCACTTCTGTCTCCTCTA
 ATAAGCCCCACCCCTCCCGCCTGGCCTCCCTGCTGCCCTGCCTGTTCCCCATTAGCACA
 GGAGTAGCAGCAGCAGGACAGGCAAGAGCCTCACAAAGTGGACTCTGGCCTCTGACCAGCT
 GTGCGGCATGGCTAACGTCACTGCCCTCGGAGCCTCTGGAAGCTAGGGCACATTGGTT
 CCAGCCTAGCCAGTTCTACCCCTGGGTGGGTCAGCATCCAGACTGGAAACCTACC
 CATTTCCCCTGAGCATCCTCTAGATGCTGCCCAAGGAGTGTGCAAGTCTGGAGCCTCA
 TCTGGCTGGATCTCAAGGGCCTCTGGATTCAAGTCCCTGAGCAGACAGC
 CCTTCTTACCCCTCCAGGAATGCCGTGAAAGGAGACAAGGTCTGCCGACCCATGTCTATGC
 TCTACCCCCAGGGCAGCATCTCAGCTTCCGAACCCCTGGCTGTTCTTAGTCTTCA
 TAAAAGTTGTTGCCCTTTAACGGAGTGTCACTTCAACCGCCCTCCCTACCCCTGCTGGC
 CGGGGATGGAGACATGTCAATTGTAAGCAGAAAAAGGTTGCATTGTTCACTTTGTAAT
 ATTGTCTGGGCTGTGTTGGGGTGTGGGGAGCTGGCAGTCAGTGGCCACATGGCAGTC
 AGGGGCTGGCCCCACAGAGACCCACAGGGCAGTGAAGCTGTCTTCCCCACCTGCCCTAGC
 CCATCATCTAACCGGTCTTGATTTAATAAACACTATAAAAGGTTAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAAA

FIGURE 232

```
>/usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77652
><subunit 1 of 1, 353 aa, 1 stop
><MW: 37847, pI: 6.80, NX(S/T): 2
MPWPLLLLLAVSGAQQTTRPCFPGCQCEVETFGLFDSFSLTRVDCSGLGPHIMPVPIPLDTAH
LDLSSNRLEMVNESVLAGPGYTTLAGLDLSHNLLTSISPTAFSRLRYLESLDLSHNGLTALP
AESFTSSPLSDVNLSHNQLREVSVAFTTHSQGRALHVDLSHNLIHRLVPHPTRAGLPAPTI
QSLNLAWNRLHAVPNLRDPLRVLSDLGNPLAVIGPGAFAGLGGLTHLSLASLQRQLPELAPS
GFRELPGQLVLDLSGNPKLNWAGAEVFSGLSSLQELDLSGTNLVPLPEALLHLPALQSVSV
GQDVRCRRLVREGTYPRRPGSSPKVPLHCVDTRESAARGPTIL
```

Signal peptide:

amino acids 1-16

Transmembrane domains:

amino acids 215-232, 287-304

FIGURE 233

GATGGCGCAGCCACAGCTCTGTGAGATTGATTCTCCCCAGTTCCCCTGTGGGTCTGAGG
 GGACCAAGGGTGAGCTACGTTGGCTTCTGGAAGGGGAGGCTAT**ATG**CGTCAATTCCCCA
 AAACAAGTTTGACATTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCT
 GTTCCAGGCCTTACCTGCTGGCACTAACGGCGGAGCCAGGATGGGACAGAATAAAGGAGC
 CACGACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTCTTCAC
 GGGAGGCTTGGCAGTTTCTTACTCCTGTGGTCTCCAGATTCAAGGCTAAGATGAAAGCC
 TCTAGTCTTGCCTTCAGCCTCTCTGCTGCGTTTATCTCCTATGGACTCCTCCACTGG
 ACTGAAGACACTCAATTGGAAAGCTGTGATGCCACAAACCTTCAGGAAATACGAAATG
 GATTTCTGAGATAACGGGCAGTGTGCAAGCAAAGATGAAACATTGACATCAGAATCTTA
 AGGAGGACTGAGTCTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCCATT
 GCTAAGACTCTATCTGGACAGGGTATTTAAAAACTACCAGACCCCTGACCATTATACTCTCC
 GGAAGATCAGCAGCCTGCCAATTCTTCTTACCATCAAGAAGGACCTCCGGCTCTCAT
 GCCCACATGACATGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCA
 CTTGAAAAGCTGGAACCTCAGGCAGCAGTTGTGAAGGCTTGGGGAACTAGACATTCTTC
 TGCAATGGATGGAGGAGACAGA**TAG**GAGGAAAGTGATGCTGCTGCTAAGAATATTGAGGT
 CAAGAGCTCCAGTCTCAATACCTGCAGAGGGAGGCATGACCCAAACCACCATCTTTACT
 GTACTAGTCTTGTGCTGGTCACAGTGTATCTTATTGCTACTTGCTTGCATGAT
 TGTCTTATGCATCCCCATCTTAATTGAGACCATACTGTATAAGATTTGTAATATCTT
 TCTGCTATTGGATATATTATTAGTTAATATATTATTATTGCTATTAAATGTATTT
 ATTTTTTACTGGACATGAAACTTAAAAAAATTCACAGATTATTTATAACCTGACTAG
 AGCAGGGTGTATTGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 AGGGGGGTATTCAACTAAGGACATATTACTCATGCTGATGCTCTGTGAGA
 TATTGAAATTGAACCAATGACTACTTAGGATGGGGTGTGAAATAAGTTGATGTGAAATT
 GCACATCTACCTTACAATTACTGACCACCCAGTAGACTCCCCAGTCCCATAATTGTGAT
 CTTCCAGCCAGGAATCCTACACGGCCAGCATGTATTCTACAAATAAAGTTCTTGCATA
 CCAAAAAAAAAAAAAAAA

FIGURE 234

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: .8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSELRP
EIFSSREAWQFLLLWSPDFRPKMKA S LAFSLLSAAFYLLWTPSTGLKTLNLGSCVIATNL
QEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLD RVFKNYQTP
DHYTLRKISSLANSFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQA AVVKALG
ELDILLQWMEETE
```

Important features of the protein:

Signal peptide:

amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 192-195, 225-228

N-myristoylation sites.

amino acids 42-47, 46-51, 136-141

FIGURE 235

CCGTTATCGTCTTGCCTACTGCTGAATGTCCGTCCGGAGGAGGAGGGCTTTGCCG
 CTGACCCAGAGATGGCCCCGAGCGAGCAAATTCTACTGTCCGGCTGCGCGGCTACCGTGGC
 CGAGCTAGCAACCTTCCCCTGGATCTCACAAAAACTCGACTCCAAATGCAAGGAGAACAG
 CTCTTGCTCGGTTGGGAGACGGTGCAAGAGAATCTGCCCCCTATAGGGGAATGGTGCACACA
 GCCCTAGGGATCATTGAAGAGGAAGGCTTCTAAAGCTTGGCAAGGAGTGACACCCGCCAT
 TTACAGACACGTAGTGTATTCTGGAGGTGAATGGTCACATATGAACATCTCGAGAGGTTG
 TGTTGGCAAAAGTGAAGATGAGCATTATCCCCTTGGAAATCAGTCATTGGAGGGATGATG
 GCTGGTGTATTGGCCAGTTTAGCCAATCCAACGTACCTAGTGAAGGTTCAGATGCAAAT
 GGAAGGAAAAAGGAAACTGGAAGGAAAACCATTGCGATTCTGTGGTACATCATGCATTG
 CAAAAATCTTAGCTGAAGGAGGAATACGAGGGCTTGGCAGGCTGGTACCCAATATAACAA
 AGAGCAGCACTGGTGAATATGGGAGATTAAACCACCTATGATACTGAAACACTACTTGGT
 ATTGAATAACACCACTTGAGGACAATATCATGACTCACGGTTATCAAGTTATGTTCTGGAC
 TGGTAGCTTCTATTCTGGAACACCAGCCATGTCAAAAGCAGAATAATGAATCAACCA
 CGAGATAAACAGGAAGGGACTTTGTATAAATCATCGACTGACTGCTTGATTCAAGGCTGT
 TCAAGGTGAAGGATTCATGAGTCTATATAAAGGCTTTACCATCTGGCTGAGAATGACCC
 CTTGGTCAATGGTGTCTGGCTTACTTATGAAAAAATCAGAGAGATGAGTGGAGTCAGTCCA
 TTTTAA

FIGURE 236

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77568
><subunit 1 of 1, 323 aa, 1 stop
><MW: 36064, pI: 9.33, NX(S/T): 1
MSVPEEEERLLPLTQRWPRASKFLLSGCAATVAELATFPLDLTKTRLQMGEAALARLGDGA
RESAPYRGMVRTALGIIEEGFLKLWQGVTPAIYRHVVYSGGRMVTYEHLCVFGKSEDEH
YPLWKSVIGGMMAGVIGQFLANPTDLVKVQMMEGKRKLEGKPLRFRGVHHAFAKILAEGGI
RGLWAGWVPNIQRAALVNMGDLTTYDTVKHYLVNTPLEDNIMTHGLSSLCGLVASILGTP
ADVIKSrimNQPRDKQGRGLLYKSSTDCLIQAVQGEGFMSLYKGFLPSWLRMTPWSMVFWLT
YEKIREMSGVSPF
```

Transmembrane domains:

amino acids 25-38, 130-147, 233-248

FIGURE 237

CGGACGCGTGGCGCGGGACGCCGGCAGGGTTGTGGCGCAGCAGTCCTCCTGCAGCG
 GCCTGAAGTCGGCGTGGCGTTGAGGAAGCTGGATAACAGCATTAAATGAAAAATTATGC
 TTAAGAAGTAAAATGGCAGGCTCCTAGATAATTCGTTGGCCAGAATGTGAATGTATTG
 ACTGGAGTGAGAGAAGAAATGCTGTGGCATCTGTTGCGCAGGTATATTGTTTACAGGC
 TGGTGGATAATGATTGATGCAGCTGTGGTGTATCCTAACGCCAGAACAGTTGAACCATGCC
 TCACACATGTGGTGTATTTCCACATTGGCTTCTCATGATAAAATGCTGTATCCAATGCTC
 AGGTGAGAGGTGATAGCTATGAAAGCGGCTGTTAGGAAGAACAGGTGCTCGAGTTGGCTT
 TTCATTGGTTCATGTTGATGTTGGTCACTTATTGCTTCCATGTGGATTCTTTGGTGC
 ATATGTTACCCAAAATACTGATGTTATCCGGGACTAGCTGTGTTTTCAAAATGCACTTA
 TATTTTAGCACTCTGATCTACAAATTGGAAGAACCGAAGAGCTATGGACTGAGATCAC
 TTCTTAAGTCACATTTCTTTGTTATTCTGTTGAGATAGGTTTATCTCAGT
 ACACATTGCCAAATGGAGTAGATTGTACATTAAATGTTGTTCTTACATTTATGTC
 TGAGTTGAAATAGTTATGAAATTCTTATTTCATTGCATAGACTGTTAATATGTA
 TATAATACAAGACTATATGAATTGATAATGAGTATCAGTTTTATTCCCTGAGATTAGAA
 CTTGATCTACTCCCTGAGCCAGGGTTACATCATCTGTCATTAGAAGTAACCACTCTGT
 CTCTCTGGCTGGCACGGTGGCTCATGCCGTAAATCCCAGCACTTGGGAGGCCGAGGCC
 CCGATTGCTTGAGGTCAAGTGTGTTGAGACCCAGCCTGGCAACATGGCGAAACCCC
 ATCTACT
 AAAAATACAAAAATTAGCCAGGCATGGTGGTGGTGCCTGTAATCCCAGCTACCTGGGAGGC
 TGAGGCAGGAGAATCGCTGAACCCGGGGGCAGAGGTTGCAGTGAGCTGAGTTGCCAC
 TGCACCTAGCCTGGGGAGAAAGTGAACACTCCCTCTCAAAAAAAAGACCACTCTCAGTATC
 TCTGATTCTGAAGATGTACAAAAAAATAGCTCATATATCTGGAATGAGCACTGAGCCA
 TAAAAGGTTTCAGCAAGTTGTAACCTATTTGGCTAAAAATGAGGTTTTGGTAAAGA
 AAAAATATTGTTCTTATGTATTGAAGAAGTGTACTTTATATAATGATTTTAAATGCC
 AAAGGACTAGTTGAAAGCTTCTTAAAAAGAATTCTCTAATATGACTTATGTGAGAA

FIGURE 238

MAGFLDNFRWPECECIDWSERRNAVASVAGILFFTGWWIMIDAAVVYPKPEQLNHAFHTCG
VFSTLAFFMINAVSNAQVRGDSYESGCLGRTGARVWLFIGFMLMFGSLIASMWILFGAYVTQ
NTDVYPGLAVFFQNALIFFSTLIYKFGRTEELWT

Important features:

Signal peptide:

amino acids 1-44

Transmembrane domains:

amino acids 23-42 (type II), 60-80, 97-117, 128-148

FIGURE 239

GTTGATGGCAAACCTCCTCAAAGGAGGGCAGAGCCTGCGCAGGCAGGAGCAGCTGGCCA
 CTGGCGGCCCGCAACACTCCGTCTCACCTCTGGGCCACTGCATCTAGAGGAGGGCCGTCT
 GTGAGGCCACTACCCCTCCAGCAACTGGGAGGTGGACTGTCAGAAGCTGGCCCAGGGTGGT
 GGTCAGCTGGTCAGGGACCTACGGCACCTGCTGGACCACCTCGCCTCTCCATCGAACAG
 GGAAGTGGAGCCTCGAGCCCTGGGTGGAAGCTGACCCCAAGCCACCCACCTGGACAG
GATGAGAGTGTCAGGTGTGCTCGCCTCCTGGCCCATCTTGCCATAGTCACGACATGGA
 TGTATTGAGACTACATGAGCTTCAGCATGAAAACCATCCGTCTGCCACGCTGGCTGGCA
 GCCTCGCCCACCAAGGAGATCCAGGTTAAAAGTACAAGTGTGGCCTCATCAAGCCCTGCC
 AGCCAACACTTTGCGTTAAAATCTGCAGTGGGCCAACGTCTGGCCCTACTATGT
 GCTTGAAAGACCGCATGATCATGAGTCCTGTAAAAACAAATGTGGCAGAGGCCTAACATC
 GCCCTGGTGAATGGAACCACGGAGCTGTGCTGGACAGAAGGCATTGACATGTACTCTGG
 AGATGTTATGCACCTAGTGAAATTCTTAAAGAAATTCCGGGGGTGCACTGGTGCTGGTGG
 CCTCCTACGACGATCCAGGGACCAAAATGAACGATGAAAGCAGGAAACTCTCTGACTTG
 GGGAGTTCTACGCAAACAAACTGGCTTCCGGACAGCTGGTCTTCATAGGAGCCAAAGA
 CCTCAGGGTAAAAGCCCCTTGAGCAGTTCTAAAGAACAGCCCAGACACAAACAAATACG
 AGGGATGGCCAGAGCTGGAGATGGAGGGCTGCATGCCCGAACGCCATTTAGGGTGGC
 TGTGGCTCTCCTCAGCCAGGGCCTGAAGAACGCTCCTGCCTGACTTAGGAGTCAGAGCCCG
 GCAGGGCTGAGGAGGAGGAGCAGGGGTGCTGCGTGGAAAGGTGCTGCAGGTCTGCACGC
 TGTGTCGCGCCTCTCCTCGAAACAGAACCCCTCCCACAGCACATCCTACCCGGAAGACC
 AGCCTCAGAGGGCTTCTGGAACCAGCTGTCTGGAGAGAATGGGGTGCTTCGTCAAGG
 ACTGCTGACGGCTGGTCTGAGGAAGGACAAACTGCCAGACTTGAGCCCAATTAAATTAA
 TTTTGCTGGTTTGAAAAAAAAAAAAAA

FIGURE 240

```
</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59814
<subunit 1 of 1, 224 aa, 1 stop
<MW: 24963, pI: 9.64, NX(S/T): 1
MRVSGVLRLLALIFAIVTTWMFIRSYMSFSMKTIRLPRWLAASPTKEIQVKKYKCGLIKPCP
ANYFAFKICSGAANVVGPTMCFEDRMIMSPVKNNVRGLNIALVNNTTGAVLGQKAFDMYSG
DVMHLVKFLKEIPGGALVLVASYDDPGTKMNDESRKLFDLGSYAKQLGFRDSWVFIGAKD
LRGKSPFEQFLKNSPDTNKYEGWPELLEMEGCMPPKPF
```

Important features:

Signal peptide:

amino acids 1-15

ATP/GTP-binding site motif A (P-loop) .

amino acids 184-191

N-glycosylation site.

amino acids 107-110

FIGURE 241

GAGACTGCAGAGGGAGATAAAGAGAGAGGGCAAAGAGGCAGCAAGAGATTGTCCTGGGGAT
 CCAGAAACCCATGATAACCCTACTGAACACCGAACATCCCCTGGAAGCCCACAGAGACAGAGACA
 GCAAGAGAAGCAGAGATAAATACACTCACGCCAGGAGCTCGCTCGCTCTCTCTCTCTC
 TCACTCCTCCCTCCCTCTCTCTGCCTGTCCTAGTCCTCTAGTCCTCAAATTCCCAGTCCC
 CTGCACCCCTTCCGGGACACTATGTTGTTCTCCGCCCTGCTGGAGGTGATTGGATCC
 TGGCTGCAGATGGGGTCAACACTGGACGTATGAGGGCCCACATGGTCAGGACCATTGGCCA
 GCCTCTTACCCCTGAGTGAAACAATGCCAGCTCCAGTCCACCGATATTGACAGACAGTGT
 GACATTGACCTGATTGCTGCTGCAGCCCCACGGATATGACCAGCCTGGCACCGAGC
 CTTTGGACCTGCACAACAATGCCACACAGTCAACTCTCTGCCCTTACCCGTATCTG
 GGTGGACTTCCCCGAAAATATGTAGCTGCCAGCTCCACCTGCACTGGGTAGAAAGGATC
 CCCAGGGGGTCAGAACACCAGATCAACAGTGAAGCCACATTGCAAGAGCTCCACATTGTAC
 ATTATGACTCTGATTCTATGACAGCTTGAGTGAGGCTGCTGAGAGGCCTCAGGGCTGGCT
 GTCCTGGGCATCCTAATTGAGGTGGGTGAGACTAAGAATATAGCTTATGAACACATTCTGAG
 TCACTTGCATGAAGTCAGGCATAAAGATCAGAACACCTCAGTGCCTCCCTAACCTAACAGAG
 AGCTGCTCCCCAACAGCTGGGGCAGTACTTCCGCTACAATGGCTCGCTCACAACTCCCCCT
 TGCTACCAGAGTGTGCTCTGGACAGTTTATAGAAGGTCCCAGATTCAATGGAACAGCT
 GGAAAAGCTTCAGGGGACATTGTTCTCCACAGAACAGAGGGAGCCCTCTAACGTTGGTACAGA
 ACTACCGAGCCCTCAGCCTCTCAATCAGCGCATGGCTTGTCTTCAATCCAAGCAGGA
 TCCTCGTATACCACAGGTGAAATGCTGAGTAGGTGAGGAATCTGGTTGGCTGTCTG
 CCTTCTCCTGGCTTTATTCATTGCTAGAAAGATTGGAAGAACAGGCTGGAAAACCGAA
 AGAGTGTGGTCTCACCTCAGCACAAGCCACGACTGAGGCATAAATTCTCTCAGATACCA
 TGGATGTGGATGACTTCCCTCATGCCTATCAGGAAGCCTCTAAAATGGGTGAGGATCTG
 GCCAGAAAACACTGTAGGAGTAGTAAGCAGATGTCCTCCCTGGACATCTTAGAGAG
 GAATGGACCCAGGCTGTCTTCAGGAAGAACACTGCAGAGCCTCAGCCTCTCAAACATGTA
 GGAGGAAATGAGGAAATCGCTGTGTTAATGCAGAGANCAAACCTGTTAGTTGCAGGG
 GAAGTTGGATATAACCCAAAGTCCCTACCCCCCTCACTTTATGCCCTTCCCTAGATA
 TACTGCAGGGATCTCTCCTTAGGATAAAGAGTTGCTGTTGAAGTTGTATATTTGATCAATA
 TATTGGAAATTAAAGTTCTGACTTT

FIGURE 242

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62812
><subunit 1 of 1, 337 aa, 1 stop
><MW: 37668, pI: 6.27, NX(S/T): 1
MLFSALLLEVIWILAADGGQHWTYEGPHGQDHWPASYPECGNNAQSPIDIQTDSVTFDPLP
ALQPHGYDQPGTEPLDLHNNGHTVQLSLPSTLYLGGLPRKYVAAQLHLHWGQKGSPGGSEHQ
INSEATFAELHIVHYDSDSYDSLSEAAERPQGLAVLGILIEVGETKNIAYEHILSHLHEVRH
KDQKTSVPPFNLRELLPKQLGQYFRYNGSLTPPCYQSVLWTVFYRRSQISMEQLEKLQGTL
FSTEEEPSKLLVQNYRALQPLNQRMVFASFIQAGSSYTTGEMLSLGVGILVGCLCLLLAVYF
IARKIRKKRLENRKSVVFTSAQATTEA
```

Important features of the protein:

Signal peptide:

amino acids 1-15

Transmembrane domain:

amino acids 291-310

N-glycosylation site.

amino acids 213-216

Eukaryotic-type carbonic anhydrases proteins

amino acids 197-245, 104-140, 22-69

FIGURE 243

AATTTTCACCAGAGTAAACTGAGAAACCAACTGGACCTTGAGTATTGTACATTTGCCTC
 GTGGACCCAAAGGTAGCAATCTGAAACATGAGGAGTACGATTCTACTGTTGTCTCTAGG
 ATCAACTCGGT CATT ACCACAGCTCAAACCTGCTTGGACTCCCTCCCACAAA ACTGGCTC
 CGGATCAGGAACACTACCAAACCAACAGCAGTCAAATCAGGTCTTCCTTTAAGTCTG
 ATACCATTAAACACAGATGCTCACACTGGGCCAGATCTGCATCTGTTAAATCCTGCTGCAGG
 AATGACACCTGGTACCCAGACCCACCCATTGACCCTGGAGGGTTGAATGTACAACAGCAAC
 TGCACCCACATGTGTTACCAATTTCGTACACAACTTGGAGGCCAGGGCACTATCCTAAGC
 TCAGAGGAATTGCCACAAATCTCAGGCCCTCATCATCCATTGTTCCCGGGAGGCAT
 CCTGCCACCAGTCAGGCAGGGCTAATCCAGATGCCAGGATGGAAGCCTCCAGCAGGAG
 GAGCAGGTGTAATCCTGCCACCCAGGGAACCCCAGCAGGCCCTCCAACTCCCAGTGGC
 ACAGATGACGACTTGCAGTGACCACCCCTGCAGGCATCCAAAGGAGCACACATGCCATCGA
 GGAAGCCACCACAGAATCAGCAAATGGAATTCAGTAAGCTGTTCAAATTTCAACTAAG
 CTGCCTCGAATTGGTGATA CATGTGAATCTTATCATTGATTATATTATGGAATAGATTGA
 GACACATTGGATAGTCTTAGAAGAAATTAAATTCTTAATTACCTGAAAATATTCTGAAATT
 TCAGAAAATATGTTCTATGTAGAGAATCCAACCTTTAAAACAATAATTCAATGGATAAAAT
 CTGTCTTGAAATATAACATTATGCTGCCTGGATGATATGCATATTAAAACATATTGGAAA
 ACTGGAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAA

FIGURE 244

MRSTILLFCLLGSTRSLPQLKPALGLPPTKLAPDQGTLPNQQQSNQVFPSSLIPLTQM
LTLPDLHLLNPAAGMTPGTQTHPLTLGGLNVQQQLHPHVLPFVTQLGAQGTILSSEE
LPQIFTSLIIHSLFPGGILPTSQAGANPDVQDGSLPAGGAGVNPATQGT PAGRLPTPSG
TDDDFAVTTPAGIQRSTHAIEEATTESANGIQ

Signal peptide:

amino acids 1-16

FIGURE 245

GGAGAGAGGC CGCGGGT GAAAGGCGCATTGATGCAGCCTGC GGCGCCTCGGAGCGCGCG
 GAGCCAGACGCTGACCACGTT CCTCTCCTCGGTCTCCTCCGCCTCCAGCTCCGCCTGCCCG
 GCAGCCGGAGCC **ATG** CGACCCAGGGCCCCGCCCTCCCCGCAGCGGCTCCGCCTCC
 TGCTGCTCCTGCTGCTGCAGCTGCCCGCCGT CGAGCGCCTCTGAGATCCCCAAGGGGAAG
 CAAAAGGCGCAGCTCGGCAGAGGGAGGTGGTGACCTGTATAATGGAATGTGCTTACAAGG
 GCCAGCAGGAGTGCCTGGTCGAGACGGGAGCCCTGGGGCCAATGTTATTCCGGGTACACCTG
 GGATCCCAGGT CGGGATGGATTCAAAGGAGAAAGGGGAATGTCTGAGGGAAAGCTTGAG
 GAGTCCTGGACACCCA ACTACAAGCAGT GTT CATGGAGTT CATTGA ATTATGGCATAGATCT
 TGGGAAAATTGCGGAGTGTACATTACAAGATGCGTTCAAATAGTGCTCTAACAGAGTTTGT
 TCAGTGGCTCACTCGGCTAAAATGCAGAAATGCATGCTGTCAGCGTTGGTATTCACATTC
 AATGGAGCTGAATGTT CAGGACCTCTTCCATTGAAGCTATAATTATTGGACCAAGGAAG
 CCCTGAAATGAATTCAACAATTAATATT CATCGCACTCTCTGTGGAAGGACTTGTGAAG
 GAATTGGTGCTGGATTAGTGGATGTTGCTATCTGGGTTGGCACTGTT CAGATTACCAAAA
 GGAGATGCTTCACTGGATGGAATT CAGTTCTCGCATCATTATTGAAGAACTACCAAA **TA**
AATGCTTA ATTT CATTGCTACCTCTTTTATTATGCCTT GGAATGGTTCACTTAAAT
 GACATTAAATAAGTTATGTATACATCTGAATGAAAAGCAAAGCTAAATATGTTACAGA
 CCAAAGTGTGATTCACACTGTTAAATCTAGCATTATT CATTGCTTCAATCAAAGT
 GGTTCAATATTTTTAGTTGGTTAGAATACTTCTTCATAGTCACATTCTCTCACCTA
 TAATTGGAATATTGTTGGTCTTTGTTCTTAGTATAGCATTAAAAAAATA
 TAAAAGCTACCAATCTTGTACAATTGTAAGAATT TTTTATCTGTTAAAT
 AAAAATTATTCACCAACA

FIGURE 246

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76393
><subunit 1 of 1, 243 aa, 1 stop
><MW: 26266, pI: 8.43, NX(S/T): 1
MRPQGPAAASPQRRLRGLLLLLQLPAPSSASEIPKGKQKAQLRQREVVDLYNGMCLQGPAGV
PGRDGSPGANVIPGTPGIPGRDGFKEKGECLRESFEESWTPNYKQCSWSSLNYGIDLGKIA
ECTFTKMRNSNSALRVLFSGSLRLKCRNACCQRWYFTFNGAECGPLPIEAIYLDQGSPEMN
STINIHRTSSVEGLCEGIGAGLVDVAIWVGTCSDYPKGDASTGWNSVSRIIIIEELPK

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 195-217